

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: April 16, 2004, 10:12:21 ; Search time 23 Seconds  
(without alignments)  
918.044 Million cell updates/sec

Title: US-10-063-523-22  
Perfect score: 2109  
Sequence: 1 MEGESTSAVLGFLGALAF.....TDEIEKMGGEYSRSTPT 409

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgm2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
2: /cgm2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
3: /cgm2\_6/ptodata/2/iaa/6A\_COMB.pep:\*  
4: /cgm2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
5: /cgm2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /cgm2\_6/ptodata/2/iaa/backfiles.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	778	36.9	151	4	US-09-621-976-3917
2	122	5.8	1087	4	US-09-914-259-12
3	122	5.8	2482	1	US-08-328-284-6
4	122	5.8	3248	1	US-08-353-700-1
5	122	5.8	3248	5	PCT-US95-16216-1
6	111.5	5.3	1038	4	US-08-334-179A-2
7	111.5	5.3	1038	4	US-09-908-500A-2
8	111	5.3	1972	4	US-08-875-435B-4
9	110.5	5.2	1038	3	US-09-541-782-4
10	110.5	5.2	1038	4	US-09-723-820-4
11	110.5	5.2	1038	4	US-10-270-085-4
12	110	5.2	530	4	US-08-979-608A-8
13	110	5.2	530	4	US-09-517-849-8
14	110	5.2	530	4	US-09-616-289-8
15	110	5.2	546	4	US-09-616-289-44
16	109.5	5.2	1038	4	US-08-334-179A-8
17	109	5.2	1972	4	US-08-875-435B-3
18	108.5	5.1	1257	1	US-08-049-783-2
19	108.5	5.1	1257	1	US-08-158-232-6
20	108.5	5.1	1257	1	US-08-304-626-6
21	108.5	5.1	1257	1	US-08-316-301A-6
22	108.5	5.1	1257	2	US-08-611-928-6
23	108.5	5.1	1257	3	US-09-173-891-6
24	108.5	5.1	1257	3	US-09-076-137-6
25	108.5	5.1	1257	3	US-09-738-363-6
26	108.5	5.1	1257	5	PCT-US92-03624-6
27	108.5	5.1	2662	4	US-09-595-684B-31

28	108	5.1	557	4	US-08-979-608A-5	Sequence 5, Appli
29	108	5.1	557	4	US-09-517-849-5	Sequence 5, Appli
30	108	5.1	557	4	US-09-616-289-5	Sequence 5, Appli
31	108	5.1	2954	4	US-08-150-867-1	Sequence 1, Appli
32	106.5	5.0	558	1	US-08-285-440-6	Sequence 6, Appli
33	106.5	5.0	558	1	US-08-630-349-6	Sequence 4, Appli
34	106.5	5.0	1111	4	US-09-914-259-28	Sequence 28, Appli
35	105.5	5.0	582	4	US-08-334-179A-4	Sequence 4, Appli
36	105.5	5.0	1211	4	US-09-134-001C-4820	Sequence 4820, Ap
37	105.5	5.0	1261	3	US-09-080-855-2	Sequence 2, Appli
38	105.5	5.0	1261	4	US-09-566-076-2	Sequence 2, Appli
39	105.5	5.0	3878	4	US-09-314-259-11	Sequence 11, Appli
40	105	5.0	352	4	US-09-543-681A-6618	Sequence 6618, Ap
41	105	5.0	1969	4	US-09-418-710-72	Sequence 72, Appli
42	105	5.0	1972	4	US-09-418-710-21	Sequence 21, Appli
43	104.5	5.0	2329	3	US-08-755-587-16	Sequence 16, Appli
44	104.5	5.0	3418	2	US-08-639-501-2	Sequence 2, Appli
45	104.5	5.0	3418	2	US-08-603-753D-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1  
US-09-621-976-3917  
; Sequence 3917, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 3917  
; LENGTH: 151  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: -19..-1  
US-09-621-976-3917

Query Match	36.9%;	Score	778;	DB	4;	Length	151;
Best Local Similarity	100.0%;	Pred. No.	1.9e-64;				
Matches	151;	Conservative	0;	Mismatches	0;	Indels	0;
QY	1	MEGESTSAVLGFLGALAFQHLNTSDTEGFLGVEKGNISITDSOMDDVEVYITD	60				
Db	1	MEGESTSAVLGFLGALAFQHLNTSDTEGFLGVEKGNISITDSOMDDVEVYITD	60				
QY	61	IQKYPICYQLFFYNSGGEVNEQALKKILSNVKNVGVYKFRHSDQIMTFRERLLHKN	120				
Db	61	IQKYPICYQLFFYNSGGEVNEQALKKILSNVKNVGVYKFRHSDQIMTFRERLLHKN	120				
QY	121	LOEHFSNQLVFLLTPSIITSCSTHRLH	151				
Db	121	LOEHFSNQLVFLLTPSIITSCSTHRLH	151				

RESULT 2  
US-09-914-259-12  
; Sequence 12, Application US/09914259  
; Patent No. 6495336  
; GENERAL INFORMATION:  
; APPLICANT: Makowski, Lee  
; APPLICANT: Hymen, Paul  
; APPLICANT: Williams, Mark  
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES  
; FILE REFERENCE: 8471-010-999

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OM protein - protein search, using sw model

Run on: April 16, 2004, 10:16:01 ; Search time 46 Seconds  
(without alignments)

2805.368 Million cell updates/sec

Title: US-10-063-523-22

Perfect score: 409  
Sequence: 1 MEGSSTSAVLGSFVLGALAF.....TDEBIKKKGGEYSRSTPF 409

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 6

Total number of hits satisfying chosen parameters: 5503

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database :

SPTREMBL 25.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertibrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_ivirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	263	64.3	300	4 Q9H811	Q9H811 homo sapien
2	238	58.2	300	4 Q9H9N4	Q9H9N4 homo sapien
3	19	4.6	212	11 Q8BT69	Q8BT69 mus musculus
4	19	4.6	261	11 Q8BFV6	Q8BFV6 mus musculus
5	19	4.6	407	11 Q8BP28	Q8BP28 mus musculus
6	16	3.9	298	11 Q8K2T7	Q8K2T7 mus musculus
7	9	2.2	546	17 Q28405	Q28405 archaeoglob
8	8	2.0	128	16 Q83R71	Q83R71 shigella fl
9	8	2.0	132	15 Q8AD48	Q8AD48 human immun
10	8	2.0	246	16 Q8VD88	Q8VD88 bruceella me
11	8	2.0	250	16 Q8FUN2	Q8FUN2 bruceella su
12	8	2.0	297	16 Q9A4B6	Q9A4B6 caulobacter
13	8	2.0	301	4 Q8NCW9	Q8NCW9 homo sapien
14	8	2.0	312	3 Q94401	Q94401 schizosacch
15	8	2.0	322	6 Q28621	Q28621 oryctolagus
16	8	2.0	326	12 Q9IP73	Q9IP73 human rotav

17	8	2.0	359	4 Q9H297	Q9H297 homo sapien
18	8	2.0	360	6 Q9GK69	Q9GK69 oryctolagus
19	8	2.0	402	6 Q28622	Q28622 oryctolagus
20	8	2.0	419	4 Q15018	Q15018 homo sapien
21	8	2.0	442	16 Q8UBL9	Q8UBL9 agrobacteri
22	8	2.0	452	4 Q9Y681	Q9Y681 homo sapien
23	8	2.0	470	10 Q9M306	Q9M306 arabidopsis
24	8	2.0	639	6 Q28623	Q28623 oryctolagus
25	8	2.0	690	4 Q9HCH1	Q9HCH1 homo sapien
26	8	2.0	892	16 Q7V419	Q7V419 prochloroco
27	8	2.0	1309	10 Q9LUG9	Q9LUG9 arabidopsis
28	8	2.0	1309	10 Q8GZA2	Q8GZA2 arabidopsis
29	7	1.7	81	2 P72388	P72388 staphylococ
30	7	1.7	88	15 Q9OA88	Q9OA88 human immun
31	7	1.7	88	15 Q9DR26	Q9DR26 human immun
32	7	1.7	91	15 Q90BJ1	Q90BJ1 human immun
33	7	1.7	92	16 Q9KF07	Q9KF07 bacillus ha
34	7	1.7	100	10 Q93ZJ3	Q93ZJ3 arabidopsis
35	7	1.7	101	16 Q8NLO5	Q8NLO5 xanthomonas
36	7	1.7	103	10 Q9LTQ1	Q9LTQ1 arabidopsis
37	7	1.7	104	16 Q8ZIX9	Q8ZIX9 yersinia pe
38	7	1.7	105	16 Q8XGT8	Q8XGT8 salmonella
39	7	1.7	108	10 Q9LWQ0	Q9LWQ0 oryza sativ
40	7	1.7	110	16 Q8E6E9	Q8E6E9 streptococ
41	7	1.7	114	16 Q8A302	Q8A302 bacteroides
42	7	1.7	115	15 Q7ZEP5	Q7ZEP5 human immun
43	7	1.7	116	12 Q8V6V7	Q8V6V7 halovirus h
44	7	1.7	116	12 Q7TDP0	Q7TDP0 halovirus h
45	7	1.7	136	16 Q8Y4K1	Q8Y4K1 listeria mo
46	7	1.7	136	17 Q9UZRS	Q9UZRS pyrococcus
47	7	1.7	137	17 Q8U1N2	Q8U1N2 pyrococcus
48	7	1.7	138	16 Q93MB9	Q93MB9 clostridium
49	7	1.7	140	5 Q9XX55	Q9XX55 caenorhabdi
50	7	1.7	143	2 Q9S8S4	Q9S8S4 plesiomonas
51	7	1.7	144	16 Q99F14	Q99F14 bradyrhizob
52	7	1.7	145	16 Q8EB62	Q8EB62 shewanella
53	7	1.7	153	16 Q8UIG7	Q8UIG7 agrobacteri
54	7	1.7	153	16 Q8D1E4	Q8D1E4 yersinia pe
55	7	1.7	154	16 Q8GSG7	Q8GSG7 rhizobium l
56	7	1.7	154	16 Q92SJ9	Q92SJ9 rhizobium m
57	7	1.7	154	16 Q8YEUI	Q8YEUI bruceella me
58	7	1.7	154	16 Q8G2Z6	Q8G2Z6 bruceella su
59	7	1.7	155	2 Q9AKF2	Q9AKF2 rickettsia
60	7	1.7	156	10 Q9LIZ1	Q9LIZ1 oryza sativ
61	7	1.7	158	2 Q9RN96	Q9RN96 streptococ
62	7	1.7	173	8 Q94UY8	Q94UY8 pluvialis s
63	7	1.7	173	8 Q958D2	Q958D2 tinamus maj
64	7	1.7	174	8 Q958A6	Q958A8 pterocnem
65	7	1.7	177	12 Q57255	Q57255 vaccinia vi
66	7	1.7	181	12 Q8QMP4	Q8QMP4 cowpox viru
67	7	1.7	181	12 Q9JFT2	Q9JFT2 ectromelia
68	7	1.7	181	16 Q8RDX5	Q8RDX5 thermoanaer
69	7	1.7	182	12 Q8V4S0	Q8V4S0 monkeypox v
70	7	1.7	182	12 Q8KGA1	Q8KGA1 vaccinia vi
71	7	1.7	182	12 Q72743	Q72743 cowpox viru
72	7	1.7	185	10 Q22194	Q22194 arabidopsis
73	7	1.7	187	10 Q93674	Q93674 medicago sa
74	7	1.7	190	16 Q9K8Q2	Q9K8Q2 bacillus ha
75	7	1.7	201	5 Q8SW02	Q8SW02 encephalito
76	7	1.7	202	5 Q77378	Q77378 plasmodium
77	7	1.7	216	5 Q9X9M4	Q9X9M4 leishmania
78	7	1.7	220	2 Q9A436	Q9A436 streptococ
79	7	1.7	221	17 Q8UOK7	Q8UOK7 pyrococcus
80	7	1.7	227	16 Q8ED42	Q8ED42 shewanella
81	7	1.7	228	5 Q01329	Q01329 caenorhabdi
82	7	1.7	236	16 Q8Y2U4	Q8Y2U4 raietonia s
83	7	1.7	237	16 Q9K6G9	Q9K6G9 bacillus ha
84	7	1.7	239	5 Q9N7Q3	Q9N7Q3 lymanaea sta
85	7	1.7	242	16 Q816W1	Q816W1 bacillus ce
86	7	1.7	244	11 Q8KIL4	Q8KIL4 mus musculus
87	7	1.7	244	11 Q9J150	Q9J150 mus musculus
88	7	1.7	245	6 Q95LW2	Q95LW2 macaca fasc
89	7	1.7	245	10 Q9SNW9	Q9SNW9 arabidopsis

90	7	1.7	247	5	QBIB21	Q81b21 plasmodium	163	7	1.7	393	10	O64911	O64911 solanum tub
91	7	1.7	247	16	Q82VV9	Q82vv9 nitrosomona	164	7	1.7	395	16	Q8RA61	Q8ra61 thermoanaer
92	7	1.7	254	16	Q97J11	Q97j11 clostridium	165	7	1.7	397	16	Q81SN9	Q81sn9 bacillus an
93	7	1.7	257	16	Q97Q44	Q97q44 streptococc	166	7	1.7	398	2	O87105	O87105 streptococc
94	7	1.7	258	2	Q9AL12	Q9all2 escherichia	167	7	1.7	398	2	O87108	O87108 streptococc
95	7	1.7	264	2	Q7WZ08	Q7wz08 lysobacter	168	7	1.7	398	2	Q9R7M5	Q9r7m5 streptococc
96	7	1.7	266	16	Q97QX9	Q97qx9 streptococc	169	7	1.7	398	2	O87103	O87103 streptococc
97	7	1.7	266	16	Q8ZJC0	Q8zjc0 yersinia pe	170	7	1.7	398	2	Q9R7M8	Q9r7m8 streptococc
98	7	1.7	269	10	Q9LH18	Q9lnh8 arabidopsis	171	7	1.7	398	2	Q9R7M7	Q9r7m7 streptococc
99	7	1.7	270	16	Q8D8F1	Q8d8f1 vibrio vuln	172	7	1.7	400	4	Q7Z495	Q7z495 homo sapien
100	7	1.7	278	16	Q8PD22	Q8pe22 xanthomonas	173	7	1.7	401	10	Q810S6	Q810s6 drosophila
101	7	1.7	278	16	Q8CWG3	Q8cwg3 yersinia pe	174	7	1.7	401	16	Q84Y17	Q84y17 solanum tub
102	7	1.7	279	16	Q8PO20	Q8pzo20 xanthomonas	175	7	1.7	401	16	Q7V969	Q7v969 prochlorococ
103	7	1.7	282	10	Q9ZEL8	Q9zpl8 lotus japon	176	7	1.7	404	16	O84Z59	O84z59 chlamydia t
104	7	1.7	283	8	Q9B8U7	Q9b8u7 schistosoma	177	7	1.7	404	16	Q8XZ64	Q8xz64 ralstonia s
105	7	1.7	283	8	Q9B894	Q9b894 schistosoma	178	7	1.7	406	16	O894W1	O894w1 clostridium
106	7	1.7	283	11	Q8BIB1	Q8bib1 mus musculu	179	7	1.7	410	16	Q83X68	Q83x68 streptomyce
107	7	1.7	285	5	Q8EAG1	Q8eag1 dictyosteli	180	7	1.7	410	16	Q8ZIS2	Q8zis2 yersinia pe
108	7	1.7	285	10	O82587	O82587 arabidopsis	181	7	1.7	410	16	Q9VPG5	Q9vpg5 drosophila
109	7	1.7	291	2	Q8S810	O85810 borrelia bu	182	7	1.7	418	16	Q8RFW2	Q8rfw2 fusobacteri
110	7	1.7	291	2	Q8RAC1	Q8rac1 borrelia bu	183	7	1.7	418	16	Q9VPG4	Q9vpg4 drosophila
111	7	1.7	294	10	Q8S330	Q8s330 acetabulari	184	7	1.7	419	5	Q9W3C3	Q9w3c3 drosophila
112	7	1.7	294	16	Q8S9R3	Q8s9r3 clostridium	185	7	1.7	425	16	O82TU8	O82tu8 nitrosomona
113	7	1.7	298	8	Q9B8G3	Q9b8g3 heterodoxus	186	7	1.7	425	16	Q88EL9	Q88el9 rhizobium l
114	7	1.7	304	17	Q9HNT9	Q9hnt9 halobacteri	187	7	1.7	427	16	Q8E7Q0	Q8e7q0 streptococc
115	7	1.7	310	2	O52743	O52743 streptococc	188	7	1.7	427	16	Q8E292	Q8e292 streptococc
116	7	1.7	310	2	O87F45	O8vp49 streptococc	189	7	1.7	427	16	O8CWZ6	O8cwz6 streptococc
117	7	1.7	310	2	Q9JN72	Q9jn72 streptococc	190	7	1.7	429	5	Q9SU65	Q9su65 drosophila
118	7	1.7	310	2	O52740	O52740 streptococc	191	7	1.7	431	16	O88U19	O88u19 lactobacill
119	7	1.7	310	2	O52739	O52739 streptococc	192	7	1.7	432	16	Q9PND9	Q9pnd9 campylobact
120	7	1.7	310	2	O52738	O52738 streptococc	193	7	1.7	436	16	O82KH5	O82kh5 salmonella
121	7	1.7	314	9	Q7Y547	Q7y547 bacterioph	194	7	1.7	436	16	O821T2	O821t2 salmonella
122	7	1.7	316	5	Q9VWL5	Q9vml5 drosophila	195	7	1.7	437	16	O8EFL1	O8efl1 xyliella fas
123	7	1.7	319	4	O80477	O80477 homo sapien	196	7	1.7	437	16	Q87BE0	Q87be0 xyliella fas
124	7	1.7	321	11	O70267	O70267 rattus norv	197	7	1.7	441	16	O821M1	O821m1 chlamydomoph
125	7	1.7	322	17	Q97UG4	Q97ug4 sulfolobus	198	7	1.7	446	16	O8PIY7	O8piy7 xanthomonas
126	7	1.7	322	16	Q8E515	Q8e515 streptococc	199	7	1.7	451	16	O81T41	O81t41 bacillus an
127	7	1.7	324	16	Q8DZT8	Q8dz8 streptococc	200	7	1.7	452	2	O8RPH3	O8rph3 desulfitoba
128	7	1.7	324	16	Q8DZT8	Q8dz8 streptococc	201	7	1.7	452	16	O83DC6	O83dc6 coxiella bu
129	7	1.7	324	16	Q7WQH6	Q7wqh6 bordetella	202	7	1.7	452	16	O81FY2	O81fy2 bacillus ce
130	7	1.7	324	16	Q7WCH1	Q7wch1 bordetella	203	7	1.7	452	17	Q974T6	Q974t6 sulfolobus
131	7	1.7	327	8	Q9C8S8	Q9c8s8 naegleria g	204	7	1.7	457	5	O8VBD0	O8vbd0 leishmania
132	7	1.7	329	3	Q9L110	Q9l110 oncorhynch	205	7	1.7	459	11	Q8VC86	Q8vc86 mus musculu
133	7	1.7	331	13	Q8JIC9	Q8jic9 oncorhynch	206	7	1.7	462	16	O8S5P0	O8s5p0 fusobacteri
134	7	1.7	332	10	Q8GZV9	Q8gzv9 oryza sativ	207	7	1.7	463	5	Q19311	Q19311 caenorhabdi
135	7	1.7	334	4	Q9NR44	Q9nr44 homo sapien	208	7	1.7	467	16	O87144	O87144 vibrio para
136	7	1.7	334	13	Q80U1T9	Q80u1t9 brachydanio	209	7	1.7	471	10	O9FX18	O9fx18 arabidopsis
137	7	1.7	345	13	O801T9	O801t9 brachydanio	210	7	1.7	475	10	O9M3D9	O9m3d9 arabidopsis
138	7	1.7	346	16	Q89L60	O89l60 bradyrhizob	211	7	1.7	480	16	O9K1A8	O9k1a8 neisseria m
139	7	1.7	350	5	O8SVL1	O8svl1 encephalito	212	7	1.7	481	16	O9JSL8	O9jsl8 neisseria m
140	7	1.7	351	9	O80202	O80202 methanobact	213	7	1.7	481	16	O82TV6	O82tv6 nitrosomona
141	7	1.7	351	16	Q81B65	Q81b65 bacillus ce	214	7	1.7	483	17	O59623	O59623 pyrococcus
142	7	1.7	357	4	O15338	O15338 homo sapien	215	7	1.7	490	2	O83X65	O83x65 streptomyce
143	7	1.7	357	16	Q88H70	Q88h70 pseudomonas	216	7	1.7	491	13	O9PU40	O9pu40 gallus gall
144	7	1.7	359	4	P78410	P78410 homo sapien	217	7	1.7	494	8	O85YP3	O85yp3 chlamysee
145	7	1.7	359	10	O81IJ0	O81ij0 oryza sativ	218	7	1.7	494	16	O7WCV2	O7wcv2 bordetella
146	7	1.7	359	11	Q9EQ03	Q9eq03 mus musculu	219	7	1.7	494	16	O7W5C0	O7w5c0 bordetella
147	7	1.7	361	5	O44157	O44157 caenorhabdi	220	7	1.7	494	16	O7VZP2	O7vzp2 bordetella
148	7	1.7	361	12	O84574	O84574 paramesum	221	7	1.7	497	2	Q9Z6C9	Q9z6c9 lactobacill
149	7	1.7	362	17	O8TN83	O8tn83 methanosarc	222	7	1.7	508	11	Q8BVH7	Q8bvh7 mus musculu
150	7	1.7	366	2	O8RT95	O8rt95 streptococc	223	7	1.7	512	5	O9NNZ1	O9nnz1 drosophila
151	7	1.7	367	17	Q978X8	Q978x8 thermoplasm	224	7	1.7	517	17	Q97BE6	Q97be6 thermoplasm
152	7	1.7	371	16	Q985Z4	Q985z4 rhizobium l	225	7	1.7	527	2	O70037	O70037 streptococc
153	7	1.7	373	13	Q7SYD4	Q7syd4 brachydanio	226	7	1.7	529	16	O89DN8	O89dn8 bradyrhizob
154	7	1.7	378	2	O8KUG7	O8kug7 actinomyce	227	7	1.7	536	10	O81516	O81516 arabidopsis
155	7	1.7	380	5	O9VPF7	O9vpf7 drosophila	228	7	1.7	538	16	O83B46	O83b46 coxiella bu
156	7	1.7	385	10	O80521	O80521 arabidopsis	229	7	1.7	540	2	O81EL4	O81el4 bacillus ce
157	7	1.7	386	16	O50729	O50729 borrelia bu	230	7	1.7	540	2	O87689	O87689 bacillus me
158	7	1.7	387	16	O82B97	O82b97 streptomyce	231	7	1.7	564	16	Q9X144	Q9x144 thermotoga
159	7	1.7	391	16	O81KT4	O81kt4 bacillus an	232	7	1.7	567	16	O8RIE2	O8rie2 fusobacteri
160	7	1.7	391	16	O81FJ9	O81fj9 bacillus ce	233	7	1.7	567	16	O81289	O81289 plasmodium
161	7	1.7	391	16	O817A5	O817a5 bacillus ce	234	7	1.7	568	5	Q869X0	Q869x0 dictyosteli
162	7	1.7	392	16	O82XZ1	O82xz1 nitrosomona	235	7	1.7	572	16	Q9PBK4	Q9pbk4 xyliella fas

236	7	1.7	572	16	Q87C92	Q87C92 xylella fas	309	7	1.7	1375	4	Q8IX65	Q8IX65 homo sapien
237	7	1.7	573	5	Q97211	Q97211 leishmania	310	7	1.7	1378	4	Q8WXR4	Q8WXR4 homo sapien
238	7	1.7	583	16	Q8YN55	Q8YN55 anabaena sp	311	7	1.7	1388	4	Q8IZA8	Q8IZA8 homo sapien
239	7	1.7	588	2	Q8GPLL	Q8GPLL streptococc	312	7	1.7	1314	4	Q8IX66	Q8IX66 homo sapien
240	7	1.7	588	2	Q8GPK6	Q8GPK6 streptococc	313	7	1.7	1330	10	Q8LI60	Q8LI60 oryza sativ
241	7	1.7	589	16	Q8UIZ5	Q8UIZ5 agrobacteri	314	7	1.7	1341	4	Q8IX67	Q8IX67 homo sapien
242	7	1.7	591	11	Q8OWU4	Q8OWU4 mus musculu	315	7	1.7	1346	10	Q8GU60	Q8GU60 oryza sativ
243	7	1.7	593	5	Q8TSL2	Q8TSL2 anopheles g	316	7	1.7	1353	4	Q9Y4B5	Q9Y4B5 homo sapien
244	7	1.7	608	2	Q84951	Q84951 streptococc	317	7	1.7	1357	10	Q8GU61	Q8GU61 oryza sativ
245	7	1.7	617	16	Q32206	Q32206 bacillus su	318	7	1.7	1388	13	Q91785	Q91785 xenopus lae
246	7	1.7	618	16	Q8P6Q2	Q8P6Q2 xanthomonas	319	7	1.7	1426	10	Q8L4X0	Q8L4X0 oryza sativ
247	7	1.7	635	2	Q1L9G7	Q1L9G7 streptomyc	320	7	1.7	1451	11	Q91ZD9	Q91ZD9 ratu
248	7	1.7	642	16	Q8A2G4	Q8A2G4 bacteroides	321	7	1.7	1496	4	Q9H226	Q9H226 homo sapien
249	7	1.7	651	17	Q9YCF0	Q9YCF0 aeropyrum p	322	7	1.7	1496	11	Q91ZD8	Q91ZD8 ratu
250	7	1.7	661	16	Q88BG8	Q88BG8 pseudomonas	323	7	1.7	1568	4	Q6O486	Q6O486 homo sapien
251	7	1.7	674	16	Q9HT30	Q9HT30 pseudomonas	324	7	1.7	1574	11	Q9QZC2	Q9QZC2 mus musculu
252	7	1.7	675	16	Q7U958	Q7U958 synechococc	325	7	1.7	1667	5	Q18901	Q18901 caenorhabdi
253	7	1.7	689	17	Q26380	Q26380 methanobact	326	7	1.7	1669	11	Q9QZS0	Q9QZS0 mus musculu
254	7	1.7	693	17	Q799A5	Q799A5 thermoplasm	327	7	1.7	1670	12	Q9IR67	Q9IR67 cucumbe
255	7	1.7	714	16	Q87HC1	Q87HC1 vibrio para	328	7	1.7	1670	12	Q91LR4	Q91LR4 zucchini
256	7	1.7	718	5	Q9NEM5	Q9NEM5 caenorhabdi	329	7	1.7	1670	12	Q91E49	Q91E49 kyuri green
257	7	1.7	719	2	Q9RET3	Q9RET3 streptococc	330	7	1.7	1672	16	Q8Y366	Q8Y366 rai
258	7	1.7	727	5	Q57114	Q57114 streptococc	331	7	1.7	1919	10	Q8LRK9	Q8LRK9 arabidopsi
259	7	1.7	727	5	Q17436	Q17436 caenorhabdi	332	7	1.7	1994	10	Q9LP19	Q9LP19 arabidopsi
260	7	1.7	728	17	Q59093	Q59093 pyrococcus	333	7	1.7	2838	16	Q891C5	Q891C5 clostridium
261	7	1.7	731	4	Q84099	Q84099 homo sapien	334	7	1.7	3013	5	Q8IJZ5	Q8IJZ5 plasmodium
262	7	1.7	743	16	Q87Y23	Q87Y23 pseudomonas	335	7	1.7	3507	16	Q7UNR7	Q7UNR7 rhodopirell
263	7	1.7	745	11	Q7TS74	Q7TS74 mus musculu	336	7	1.7	3770	16	Q87G75	Q87G75 vibrio para
264	7	1.7	749	11	Q8BXW0	Q8BXW0 mus musculu	337	7	1.7	4293	11	Q88852	Q88852 mus musculu
265	7	1.7	754	16	Q89V88	Q89V88 bradyrhizob	338	7	1.7	8081	5	Q7Z120	Q7Z120 caenorhabdi
266	7	1.7	764	10	Q49371	Q49371 arabidopsi	339	7	1.7	9196	5	Q8IQ87	Q8IQ87 drosophila
267	7	1.7	767	13	Q91215	Q91215 oncorhynch	340	7	1.7	10061	5	Q8I3Z1	Q8I3Z1 plasmodium
268	7	1.7	775	5	Q9Y015	Q9Y015 plasmodium	341	7	1.7	19	4	Q8WTX6	Q8WTX6 homo sapien
269	7	1.7	781	2	Q52753	Q52753 ruminococc	342	7	1.7	29	16	Q8ZQW0	Q8ZQW0 salmonella
270	7	1.7	783	10	Q8H185	Q8H185 arabidopsi	343	7	1.7	29	16	Q8X2E5	Q8X2E5 escherichia
271	7	1.7	783	10	Q9C5L5	Q9C5L5 arabidopsi	344	7	1.7	35	16	Q7UGL8	Q7UGL8 rhodopirell
272	7	1.7	783	17	Q8TT99	Q8TT99 methanosa	345	7	1.7	36	16	Q87GE2	Q87GE2 vibrio para
273	7	1.7	784	16	Q87R57	Q87R57 streptococc	346	7	1.7	39	16	Q7UQD8	Q7UQD8 rhodopirell
274	7	1.7	784	16	Q8DQ30	Q8DQ30 streptococc	347	7	1.7	45	10	P82191	P82191 spinacia ol
275	7	1.7	785	10	Q23072	Q23072 arabidopsi	348	7	1.7	45	16	Q8F630	Q8F630 leptospira
276	7	1.7	794	5	Q8MMJ4	Q8MMJ4 strongyloce	349	7	1.7	45	16	Q87G00	Q87G00 vibrio para
277	7	1.7	796	16	Q8A5U3	Q8A5U3 bacteroides	350	7	1.7	46	4	Q9N141	Q9N141 homo sapien
278	7	1.7	810	12	Q8JS13	Q8JS13 phthorimaea	351	7	1.7	46	16	Q8EIS6	Q8EIS6 shewanella
279	7	1.7	811	10	Q9SPF2	Q9SPF2 arabidopsi	352	7	1.7	47	16	Q9RJN2	Q9RJN2 streptomyc
280	7	1.7	817	5	Q8BLL1	Q8BLL1 caenorhabdi	353	7	1.7	47	16	Q8Z2V1	Q8Z2V1 enterococc
281	7	1.7	827	11	Q8CFM7	Q8CFM7 mesocricetu	354	7	1.7	49	2	Q9EVO6	Q9EVO6 escherichia
282	7	1.7	860	12	Q9WZ66	Q9WZ66 melanoplus	355	7	1.7	52	12	Q7T702	Q7T702 equine rota
283	7	1.7	864	10	Q9ZT97	Q9ZT97 arabidopsi	356	7	1.7	52	12	Q7T6Z7	Q7T6Z7 equine rota
284	7	1.7	869	5	Q94174	Q94174 caenorhabdi	357	7	1.7	53	8	Q34180	Q34180 cepaea nemo
285	7	1.7	873	10	Q84YV7	Q84YV7 oryza sativ	358	7	1.7	55	5	Q7YVY2	Q7YVY2 trypanosoma
286	7	1.7	878	4	Q86TB1	Q86TB1 homo sapien	359	7	1.7	55	10	Q88688	Q88688 zea mays (m
287	7	1.7	897	5	Q9V329	Q9V329 caenorhabdi	360	7	1.7	58	16	Q7UF91	Q7UF91 rhodopirell
288	7	1.7	897	5	Q9V329	Q9V329 drosophila	361	7	1.7	58	16	Q7UF91	Q7UF91 rhodopirell
289	7	1.7	903	5	Q8LDV9	Q8LDV9 plasmodium	362	7	1.7	59	2	Q57397	Q57397 borrelia af
290	7	1.7	913	16	Q822C0	Q822C0 chlamydophi	363	7	1.7	60	4	Q86W00	Q86W00 homo sapien
291	7	1.7	914	11	Q8CFM8	Q8CFM8 mesocricetu	364	7	1.7	60	10	Q9LFB7	Q9LFB7 arabidopsi
292	7	1.7	914	17	Q8TPC2	Q8TPC2 methanosa	365	7	1.7	60	16	Q8F7Z5	Q8F7Z5 leptospira
293	7	1.7	950	5	Q9Y100	Q9Y100 drosophila	366	7	1.7	61	16	Q89UG3	Q89UG3 staphylococ
294	7	1.7	972	2	Q83448	Q83448 enterococc	367	7	1.7	62	10	Q8XFY0	Q8XFY0 chlorella p
295	7	1.7	1053	10	Q4E822	Q4E822 oryza sativ	368	7	1.7	62	16	Q8XLY5	Q8XLY5 bacillus an
296	7	1.7	1053	10	Q4E822	Q4E822 oryza sativ	369	7	1.7	62	16	Q817Y6	Q817Y6 bacillus ce
297	7	1.7	1065	16	Q820K6	Q820K6 nitrosomona	370	7	1.7	63	14	Q95IT4	Q95IT4 uncultured
298	7	1.7	1080	5	Q81BB2	Q81BB2 plasmodium	371	7	1.7	63	16	Q88AJ8	Q88AJ8 pseudomonas
299	7	1.7	1087	5	Q96923	Q96923 dictyosteli	372	7	1.7	64	2	Q9EV37	Q9EV37 legionella
300	7	1.7	1099	16	Q8FTW9	Q8FTW9 corynebacte	373	7	1.7	64	17	Q97XF7	Q97XF7 sulfolobus
301	7	1.7	1113	4	Q96N94	Q96N94 homo sapien	374	7	1.7	64	2	Q9F2D2	Q9F2D2 salmonella
302	7	1.7	1121	12	Q84405	Q84405 peanut bud	375	7	1.7	67	2	Q9F2D2	Q9F2D2 trypanosoma
303	7	1.7	1166	12	Q9CNC4	Q9CNC4 cucumber gr	376	7	1.7	67	5	Q7YUP9	Q7YUP9 trypanosoma
304	7	1.7	1166	12	Q91E48	Q91E48 kyuri green	377	7	1.7	67	10	Q8LRY4	Q8LRY4 oryza sativ
305	7	1.7	1166	12	Q911R3	Q911R3 zucchini gr	378	7	1.7	67	12	Q9SES1	Q9SES1 kaposi's sa
306	7	1.7	1192	4	Q8IX64	Q8IX64 homo sapien	379	7	1.7	67	16	Q8FJV2	Q8FJV2 escherichia
307	7	1.7	1205	11	Q8CGW1	Q8CGW1 mus musculu	380	7	1.7	69	16	Q8KFA2	Q8KFA2 chlorobium
308	7	1.7	1251	4	Q8IX68	Q8IX68 homo sapien	381	7	1.7	69	16	Q8KFA1	Q8KFA1 chlorobium



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382 1.5 69 16 Q8KF99 chlorobium
383 1.5 72 16 Q98MR4 rhizobium l
384 1.5 72 16 Q98JN6 rhizobium l
385 1.5 74 16 Q98G7 thermoanaer
386 1.5 75 4 Q86TT7 homo sapien
387 1.5 75 10 Q7XYC7 triticum ae
388 1.5 75 12 Q8VBF3 white spot
389 1.5 76 4 Q86UW4 homo sapien
390 1.5 76 4 Q86TH9 homo sapien
391 1.5 77 16 Q8XU7 ralestonia s
392 1.5 78 2 Q8RMZ3 helicobacte
393 1.5 78 16 Q9ASE1 cryza sativ
394 1.5 79 16 Q89NV1 bradyrhizob
395 1.5 79 16 Q82RS4 streptomyc
396 1.5 80 8 Q47957
397 1.5 80 12 Q93305 porcine rep
398 1.5 81 4 Q6P80 homo sapien
399 1.5 81 11 Q99LK5 mus musculu
400 1.5 82 2 Q9APU8 pseudomonas
401 1.5 82 17 Q97513 sulfolobus
402 1.5 84 11 Q8K517 mus musculu
403 1.5 84 16 Q9JVG8 neisseria m
404 1.5 85 2 Q9461 mycoplasma
405 1.5 86 12 Q990R4 hepatitis c
406 1.5 89 2 Q45014 borrelia bu
407 1.5 89 12 Q55735 chilo iride
408 1.5 89 13 Q800D0 salvelinus
409 1.5 90 10 Q9F82 cryza sativ
410 1.5 90 12 Q8QL19 sulfolobus
411 1.5 90 16 Q9PB24 xylolla fas
412 1.5 90 16 Q87BU4 xylolla fas
413 1.5 91 16 Q8PN38 xanthomonas
414 1.5 91 16 Q8XF33 salmonella
415 1.5 91 16 Q83732 enterococcu
416 1.5 92 10 Q8M306 silene coni
417 1.5 92 10 Q42488 pharbitis n
418 1.5 93 13 Q8ETL0 platichthys
419 1.5 94 12 Q8V9M4 sulfolobus
420 1.5 94 16 Q8PB14 xanthomonas
421 1.5 95 2 Q45015 borrelia bu
422 1.5 95 9 Q8SDG4 bacterioph
423 1.5 95 15 Q9VS15 human immun
424 1.5 96 2 Q85918 ebhigomona
425 1.5 96 11 Q222B4 mus musculu
426 1.5 97 10 Q8LK32 thimopyrum
427 1.5 97 12 Q990R3 hepatitis c
428 1.5 97 12 Q990R5 hepatitis c
429 1.5 97 12 Q990R2 hepatitis c
430 1.5 97 12 Q990R0 hepatitis c
431 1.5 97 12 Q990R6 hepatitis c
432 1.5 98 5 Q86L06 dictyosteli
433 1.5 98 9 Q92XG0 bacterioph
434 1.5 98 16 Q98PG6 mycoplasma
435 1.5 99 2 Q45122 bacteroides
436 1.5 99 6 Q9XSA8 sus scrofa
437 1.5 101 4 Q86YV5 homo sapien
438 1.5 101 5 Q9N8G1 trypanosoma
439 1.5 101 5 Q7YIN0 cryptospori
440 1.5 102 1 Q07119 halobacteri
441 1.5 102 10 Q9LHZ5
442 1.5 102 10 Q8GYP9 arabidopsis
443 1.5 102 11 P97517 phodopus su
444 1.5 102 11 Q9DA17 mus musculu
445 1.5 103 10 Q9XHO9 prunus dulc
446 1.5 103 16 Q9CB6 bradyrhizob
447 1.5 104 4 Q9UHQ7 homo sapien
448 1.5 104 9 Q9B0E5 staphylococ
449 1.5 104 9 Q8SDQ2 staphylococ
450 1.5 104 10 Q04293 arabidopsis
451 1.5 104 11 Q9DD24 mus musculu
452 1.5 104 11 Q9CTI5 mus musculu
453 1.5 104 16 P73794 synechocyst
454 1.5 104 16 Q9CLF6 pasteurella

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455 1.5 104 16 Q8NWJ5 staphylococ
456 1.5 104 17 Q96XB6 sulfolobus
457 1.5 105 5 Q90514 manduca sex
458 1.5 105 17 Q27553 methanobact
459 1.5 106 2 Q8ELW9 chlorobium
460 1.5 106 5 Q917Q5 drosophila
461 1.5 107 10 Q8GS79 cryza sativ
462 1.5 107 16 Q9PLR9 chlamydia m
463 1.5 108 2 Q33851 thermus the
464 1.5 108 10 Q8RVD9 cryza sativ
465 1.5 108 10 Q94HX3 cryza sativ
466 1.5 108 11 Q7XCR4 cryza sativ
467 1.5 109 11 Q8C4S4 mus musculu
468 1.5 109 16 Q89Y15 bacteroides
469 1.5 110 16 Q96833 mycobacteri
470 1.5 110 16 Q92V18 rhizobium m
471 1.5 110 16 Q8CH50 fusobacteri
472 1.5 110 16 Q8RH50
473 1.5 111 4 Q7U2Q2 mycobacteri
474 1.5 111 4 Q9NQ12 homo sapien
475 1.5 111 10 Q84N87 cadia purpu
476 1.5 111 16 Q8XW14 ralestonia s
477 1.5 112 2 Q93FL7 citrobacter
478 1.5 112 10 Q7XEJ1 cryza sativ
479 1.5 112 11 Q8CBW0 mus musculu
480 1.5 112 12 Q91B18 budgerigar
481 1.5 112 16 Q9CCZ7 mycobacteri
482 1.5 112 16 Q8KF70 chlorobium
483 1.5 112 17 Q8ZYU3 pyrobaculum
484 1.5 113 4 Q81VY1 homo sapien
485 1.5 113 5 Q09960 caenorhabdi
486 1.5 113 16 Q92M25 rhizobium m
487 1.5 113 16 Q83DG1 coxiella bu
488 1.5 114 5 Q8MMF5 drosophila
489 1.5 114 5 Q818F9 trypanosoma
490 1.5 114 5 Q818F8 trypanosoma
491 1.5 114 8 Q97541 carduelis c
492 1.5 114 8 Q99238 carduelis c
493 1.5 114 16 Q8NRH6 corynebacte
494 1.5 115 4 Q81ZE2 homo sapien
495 1.5 115 10 Q9AWM2 cryza sativ
496 1.5 115 11 Q9DAS0 mus musculu
497 1.5 116 2 Q7WY10 streptococ
498 1.5 116 4 Q9H1A8 bacillus sp
499 1.5 116 11 Q8BN17 homo sapien
500 1.5 116 16 Q7TUC9 mus musculu prochloroco

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## ALIGNMENTS

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RESULT 1
Q9H811 PRELIMINARY; PRT; 300 AA.
ID Q9H811 AC Q9H811;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein FLJ13614.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta.
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Negai K., Sato H., Sugano S., Ishibashi T., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishii S., Kawai Y.,
RA Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Negahari K.,
RA Masuho Y., Kanehori K.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

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Query Match 4.6%; Score 19; DB 11; Length 261;  
Best Local Similarity 100.0%; Pred. No. 5.4e-11;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 VVGWYKFRHSDQIMTFRE 114  
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DB 96 VVGWYKFRHSDQIMTFRE 114  
|||||

RESULT 5  
Q8BPZ8 PRELIMINARY; PRT; 407 AA.

AC Q8BPZ8;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Hypothetical protein.  
GN 3830405G04RIK.

OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CS7BL/6J; TISSUE=Eye;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573 (2002).  
DR EMBL; AK051816; BAC34780.1; -;  
DR MGD; MGI:1917931; 3830405G04RIK.  
KW Hypothetical protein.  
SQ SEQUENCE 407 AA; 46039 MW; FB9B05A197A28C64 CRC64;

Query Match 4.6%; Score 19; DB 11; Length 407;  
Best Local Similarity 100.0%; Pred. No. 8.1e-11;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 VVGWYKFRHSDQIMTFRE 114  
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DB 96 VVGWYKFRHSDQIMTFRE 114  
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RESULT 6  
Q8KZT7 PRELIMINARY; PRT; 298 AA.

AC Q8KZT7;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Similar to hypothetical protein FLJ13614.  
GN 3830405G04RIK.

OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC029845; AAB29845.1; -;  
DR MGD; MGI:1917931; 3830405G04RIK.  
KW Hypothetical protein.  
SQ SEQUENCE 298 AA; 33669 MW; 34CD1CE3AD80B7FB CRC64;

Query Match 3.9%; Score 16; DB 11; Length 298;  
Best Local Similarity 100.0%; Pred. No. 8.7e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 EDGSLKEVHKINEMYA 220  
|||||

Db 96 EDGSLKEVHKINEMYA 111  
|||||

RESULT 7  
Q28405 PRELIMINARY; PRT; 546 AA.

ID Q28405;  
AC Q28405;  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein AF1874.  
GN AF1874.

OS Archaeoglobus fulgidus.  
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;  
OC Archaeoglobaceae; Archaeoglobus.  
OX NCBI\_TaxID=2234;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=VC-15 / DSM 4304 / ATCC 49558;  
RX MEDLINE=98049343; PubMed=9389475;  
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,  
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,  
RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyriades N.C.,  
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,  
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,  
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,  
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,  
RA Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,  
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,  
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,  
RA Venter J.C.;  
RT "The complete genome sequence of the hyperthermophilic, sulphate-  
RT reducing archaeon Archaeoglobus fulgidus.";  
RL Nature 390:364-370 (1997).  
DR EMBL; AE000973; AAB89382.1; -;  
DR PIR; A69484; A69484.  
DR TIGR; AF1874; -;  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0008026; F:ATP dependent helicase activity; IEA.  
DR GO; GO:0003676; F:nucleic acid binding; IEA.  
DR InterPro; IPR006474; Cas3\_core.  
DR InterPro; IPR001410; DEAD\_.  
DR InterPro; IPR001650; Helicase\_C.  
DR Pfam; PF00271; helicase\_C; 1.  
DR SMART; SMO0487; DEXDC; 1.  
DR SMART; SMO0490; HELICG; 1.  
DR TIGRPFAMs; TIGR01587; cas3 core; 1.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 546 AA; 62755 MW; 8A340BD6E1B0D5F3 CRC64;

Query Match 2.3%; Score 9; DB 17; Length 546;  
Best Local Similarity 100.0%; Pred. No. 3.3;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 221 SLOEELKSI 229  
|||||  
DB 62 SLOEELKSI 70  
|||||

RESULT 8  
Q83R71 PRELIMINARY; PRT; 128 AA.

ID Q83R71;  
AC Q83R71;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Putative excisionase.  
GN SFI848.

OS Shigella flexneri.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Shigella.  
OX NCBI\_TaxID=623;

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RN  SEQUENCE FROM N.A.
RC  STRAIN=301 / Serotype 2a;
RA  MEDLINE=22272406; PubMed=12384590;
RX  Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA  Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA  Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA  Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA  Xu J.;
RT  "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT  through comparison with genomes of Escherichia coli K12 and O157."
RL  Nucleic Acids Res. 30:4432-4441(2002).
DR  EMBL; AF015204; AAN43409.1; -.
KW  Complete proteome.
SQ  SEQUENCE 128 AA; 14455 MW; 5C15CF4D34FBD851 CRC64;

Query Match      2.0%; Score 8; DB 16; Length 128;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  338 ASTPQIIK 345
Db  |||||
    7 ASTPQIIK 14

RESULT 9
QBAD48  PRELIMINARY; PRT; 132 AA.
AC  Q8AD48;
DT  01-MAR-2003 (TrEMBLrel. 23, Created)
DT  01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT  01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE  Gag protein (Fragment).
OS  Human immunodeficiency virus 1.
OC  Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX  NCBI_TaxID=11876;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=97USI.NYP;
RX  MEDLINE=22290097; PubMed=12402955;
RA  Robbins K.E., Weidle P.J., Brown T.M., Saekhou A.M., Coles B.,
RA  Holmberg S.D., Folks T.M., Kalish M.L.;
RT  "Molecular Analysis in Support of an Investigation of a Cluster of
RT  HIV-1-Infected Women."
RL  AIDS Res. Hum. Retroviruses 18:1157-1161(2002).
DR  EMBL; AY098617; AAM34529.1; -.
DR  GO; GO:0005198; P:structural molecule activity; IEA.
DR  InterPro; IPR000071; Retrovir_p17.
DR  Pfam; PF00540; Gag_p17; 1.
DR  PRINTS; PR00234; HIVIMATRIX.
FT  NON_TER 132
SQ  SEQUENCE 132 AA; 14713 MW; DC15353302EA07B4 CRC64;

Query Match      2.0%; Score 8; DB 15; Length 132;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  372 ANTGSSNQ 379
Db  |||||
    120 ANTGSSNQ 127

RESULT 10
QB4DR8  PRELIMINARY; PRT; 246 AA.
AC  Q84DR8;
DT  01-MAR-2002 (TrEMBLrel. 20, Created)
DT  01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT  01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE  Taurine transport system permease protein TAUC.
GN  BME10107.
OS  Brucella melitensis.
OC  Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

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OC  Brucellaceae; Brucella.
OX  NCBI_TaxID=29459;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=16M / ATCC 23456 / Biotype 1;
RX  MEDLINE=20020109; PubMed=11756688;
RA  Delvecchio V.G., Kapatral V., Redkar R.J., Patra G., Mijer C., Los T.,
RA  Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
RA  Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltzman E.,
RA  Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA  Haelkorn R., Kyplides N., Overbeek R.;
RT  "The genome sequence of the facultative intracellular pathogen
RT  Brucella melitensis."
RL  Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
DR  EMBL; AE009649; AAL53348.1; -.
DR  PIR; AI3522; AI3522.
DR  GO; GO:0016020; C:membrane; IEA.
DR  GO; GO:0005215; P:transporter activity; IEA.
DR  GO; GO:0006810; P:transport; IEA.
DR  InterPro; IPR000515; BPD_transp.
DR  Pfam; PF00528; BPD_transp; 1.
KW  Complete proteome.
SQ  SEQUENCE 246 AA; 26410 MW; 23169AF577196634 CRC64;

Query Match      2.0%; Score 8; DB 16; Length 246;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  9 VLSGFVLG 16
Db  |||||
    63 VLSGFVLG 70

RESULT 11
Q8FUN2  PRELIMINARY; PRT; 250 AA.
AC  Q8FUN2;
DT  01-MAR-2003 (TrEMBLrel. 23, Created)
DT  01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT  01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE  Taurine ABC transporter, permease protein.
GN  BRA1188.
OS  Brucella suis.
OC  Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC  Brucellaceae; Brucella.
OX  NCBI_TaxID=29461;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=J330 / Biovar 1;
RX  MEDLINE=22247741; PubMed=12271122;
RA  Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
RA  Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,
RA  Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
RA  Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,
RA  Riedmuller S., Tetelin H., Gill S.R., White O., Salzberg S.L.,
RA  Hoover D.L., Linder L.E., Halling S.M., Boyle S.M., Fraser C.M.;
RT  "The Brucella suis genome reveals fundamental similarities between
RT  animal and plant pathogens and symbionts."
RL  Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
DR  EMBL; AE014611; AAN34346.1; -.
DR  TIGR; BRA1188; -.
DR  GO; GO:0016020; C:membrane; IEA.
DR  GO; GO:0005215; P:transporter activity; IEA.
DR  GO; GO:0006810; P:transport; IEA.
DR  InterPro; IPR000515; BPD_transp.
DR  Pfam; PF00528; BPD_transp; 1.
KW  Complete proteome.
SQ  SEQUENCE 250 AA; 26879 MW; 3EF10C2447568BB0 CRC64;

Query Match      2.0%; Score 8; DB 16; Length 250;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 9 VLGFVLG 16  
DB 63 VLGFVLG 70

RESULT 12  
Q9A4B6 PRELIMINARY; PRT; 297 AA.  
AC Q9A4B6;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Hypothetical protein CC2920.  
GN CC2920.  
OS Caulobacter crescentus.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;  
OC Caulobacteraceae; Caulobacter.  
OX NCBI\_TaxID=155892;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 19089 / CB15;  
RX MEDLINE=21173698; PubMed=11259647;  
RA Eisen J., Feldblum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,  
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,  
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,  
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,  
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,  
RA Utterback T., Tran K., Wolf A., Vamathavan J., Ermolaeva M., White O.,  
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;  
RT "Complete genome sequence of Caulobacter crescentus.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).  
DR EMBL; AE005956; AAK24882.1; -;  
DR PIR; F87610; F87610.  
DR TIGR; CC2920; -;  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 297 AA; 33149 MW; F6ED5CD697B85C0D CRC64;

Query Match 2.0%; Score 8; DB 16; Length 297;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 LLGEVKGE 40  
DB 267 LLGEVKGE 274

RESULT 13  
Q8NCW9 PRELIMINARY; PRT; 301 AA.  
AC Q8NCW9;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Hypothetical protein (Prefoldin subunit) (Fragment).  
GN DKF2P586O0324.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Uterus;  
RA Ducrest A., Lauber J., Meves H.W., Weil B., Wiemann S.;  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO THE PREFOLDIN BETA SUBUNIT FAMILY.  
DR EMBL; AL834538; CAD39194.1; -;  
DR GO; GO:0003754; F:chaperone activity; IEA.  
DR InterPro; IPR001363; F:chaperone activity; IEA.  
DR InterPro; IPR002777; PrefoldinK2.  
DR InterPro; IPR000533; Tropomyosin.  
DR Pfam; PF01920; K2; 1.  
DR PRINTS; PRO0194; TROPOMYOSIN.  
DR PROSITE; PS01255; FETUIN\_2; 1.

KW Hypothetical protein; Chaperone.  
FT NON\_TER 1  
SQ SEQUENCE 301 AA; 35048 MW; 4B1E6B92F86CB3D6 CRC64;

Query Match 2.0%; Score 8; DB 4; Length 301;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 ASLQELK 227  
DB 76 ASLQELK 83

RESULT 14  
Q94401 PRELIMINARY; PRT; 312 AA.  
AC Q94401;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Putative lectin precursor, possible vesicular protein.  
GN SPCC126.08C.  
OS Schizosaccharomyces pombe (Fission yeast).  
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
OC Schizosaccharomycetes.  
OX NCBI\_TaxID=4896;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=972h-;  
RA Murphy L., Harris D., Lyne M., Rajandream M.A., Barrell B.G.;  
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL034490; CAA22477.1; -;  
DR PIR; T40912; T40912.  
DR GeneDB SPombe; SPCC126.08c; -;  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005259; F:sugar binding; IEA.  
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.  
DR InterPro; IPR008985; ConA like\_lectin.  
DR InterPro; IPR005052; Lectin leg.  
DR Pfam; PF03388; Lectin\_leg-like; 1.  
KW Lectin.  
SQ SEQUENCE 312 AA; 35129 MW; F0F17736451ECF82 CRC64;

Query Match 2.0%; Score 8; DB 3; Length 312;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GFVLGALA 19  
DB 15 GFVLGALA 22

RESULT 15  
Q28621 PRELIMINARY; PRT; 322 AA.  
AC Q28621;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Sarcoplasmic associated protein.  
GN SLAP1.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Heart;  
RA Wigle J.T., Demchyshyn L., Sattar S., Pratt M., Tuana B.S.;  
RL "Molecular Cloning of a Novel Family of Sarcoplasmic Associated Coiled-Coil Proteins: Protein-Protein Interactions at the Cell Membrane.";  
RT Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.

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DR EMBL; U21155; AAG5598.1; -.
DR InterPro; IPR001363; Fetuin.
DR InterPro; IPR002777; PrefoldinKE2.
DR InterPro; IPR000533; Tropomyosin.
DR Pfam; PF01920; KE2; 1.
DR PRINTS; PR00194; TROPOMYOSIN.
DR PROSITE; PS01255; FETUIN_2; 1.
DR PROSITE; PR00194; TROPOMYOSIN.
DR PROSITE; PS01255; FETUIN_2; 1.
SQ SEQUENCE 322 AA; 37410 MW; 8B8C61743860D7A2 CRC64;

Query Match          2.0%; Score 8; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 ASLQELK 227
DB 96 ASLQELK 103

RESULT 16
OSIP73 PRELIMINARY; PRT; 326 AA.
AC Q9H297;
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE VP7.
OS Human rotavirus G2.
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.
OX NCBI_TaxID=73034;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TW93936;
RA Lee C.N., Zao C.L.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF044353; AAF4802.1; -.
DR InterPro; IPR001963; VP7.
DR Pfam; PF00434; VP7; 1.
DR ProDom; PD000191; VP7; 1.
DR PROSITE; PS01255; FETUIN_2; 1.
SQ SEQUENCE 326 AA; 37378 MW; B63A68262A147E6A CRC64;

Query Match          2.0%; Score 8; DB 12; Length 326;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 KESRLDLD 365
DB 312 KESRLDLD 319

RESULT 17
OSIP73 PRELIMINARY; PRT; 359 AA.
AC Q9H297;
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Sarcolemmal associated protein 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Wielowieyski P.A., Sevinc S., Guzzo R., Salih M., Wigle J.T.,
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF304450; AAG41949.1; -.
DR InterPro; IPR001363; Fetuin.

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DR InterPro; IPR002777; PrefoldinKE2.
DR InterPro; IPR000533; Tropomyosin.
DR Pfam; PF01920; KE2; 1.
DR PRINTS; PR00194; TROPOMYOSIN.
DR PROSITE; PS01255; FETUIN_2; 1.
DR PROSITE; PR00194; TROPOMYOSIN.
SQ SEQUENCE 359 AA; 41854 MW; 03E28A1F7B5DD324 CRC64;

Query Match          2.0%; Score 8; DB 4; Length 359;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 ASLQELK 227
DB 137 ASLQELK 144

RESULT 18
OSIP73 PRELIMINARY; PRT; 360 AA.
AC Q9GK69;
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Sarcolemmal associated protein 1.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Wielowieyski P.A., Sevinc S., Guzzo R., Salih M., Wigle J.T.,
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF304449; AAG41948.1; -.
DR InterPro; IPR001363; Fetuin.
DR InterPro; IPR002777; PrefoldinKE2.
DR InterPro; IPR000533; Tropomyosin.
DR Pfam; PF01920; KE2; 1.
DR PRINTS; PR00194; TROPOMYOSIN.
DR PROSITE; PS01255; FETUIN_2; 1.
DR PROSITE; PS01255; FETUIN_2; 1.
SQ SEQUENCE 360 AA; 41993 MW; 5B8C0DF9C3D1E7F9 CRC64;

Query Match          2.0%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 ASLQELK 227
DB 137 ASLQELK 144

RESULT 19
OSIP73 PRELIMINARY; PRT; 402 AA.
AC Q28622;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Sarcolemmal associated protein-2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Wigle J.T., Demchishyn L., Sattar S., Pratt M., Tuana B.S.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF304450; AAG41949.1; -.
DR InterPro; IPR001363; Fetuin.

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RT coil proteins: protein-protein interactions at the cell membrane.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U21156; AAA6596.1; -.
DR InterPro; IPR001363; Fecuin.
DR InterPro; IPR002777; PrefoldinX2.
DR InterPro; IPR005333; Tropomyosin.
DR Pfam; PF01920; KE2; 1.
DR PRINTS; PR00194; TROPOMYOSIN.
DR PROSITE; PS01255; FETUIN 2; 1.
SQ SEQUENCE 402 AA; 46382 MW; F36B1DDB52D1DF22 CRC64;

Query Match 2.0%; Score 8; DB 6; Length 402;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 ASLQELK 227
Db 176 ASLQELK 183

RESULT 20
Q15018 PRELIMINARY; PRT; 419 AA.
AC Q15018;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein KIAA0157 (Fragment).
GN KIAA0157.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=96127530; PubMed=8590280;
RA Nagase T., Seki N., Tanaka A., Ishikawa K., Nomura N.;
RT Prediction of the coding sequences of unidentified human genes. IV.
RT The coding sequences of 40 new genes (KIAA0121-KIAA0160) deduced by
RT analysis of cDNA clones from human cell line KG-1."
RL DNA Res. 2:167-174(1995).
RW EMBL; D63877; BAA09927.1; -.
KW Hypothetical protein.
PT NON_TER
SQ SEQUENCE 419 AA; 47368 MW; 50F15AB18BC29D30 CRC64;

Query Match 2.0%; Score 8; DB 4; Length 419;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 EGFLGGEV 37
Db 29 EGFLGGEV 36

RESULT 21
Q8UBL9 PRELIMINARY; PRT; 442 AA.
AC Q8UBL9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE tRNA modification GTPase.
GN THDF OR ATU2832 OR AGR C 5135.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,

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RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Doan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.,
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58."
RL Science 294:2317-2323(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58."
RL Science 294:2323-2328(2001).
DR EMBL; AE009230; AAL43813.1; -.
DR EMBL; AE008196; AAK88543.1; -.
DR PIR; AG2924; AG2924.
DR PIR; F97698; F97698.
DR GO; GO:0003924; F:GTPase activity; IEA.
DR GO; GO:0006400; P:RNA modification; IEA.
DR InterPro; IPR005289; GTP-binding_dom.
DR InterPro; IPR002917; MMR_HSR1.
DR InterPro; IPR005225; Small_GTP.
DR InterPro; IPR004520; ThdF.
DR Pfam; PF01926; MMR_HSR1; 1.
DR TIGRFAMS; TIGR00650; MG442; 1.
DR TIGRFAMS; TIGR00231; small_GTP; 1.
DR TIGRFAMS; TIGR00450; thdF; 1.
KW Complete proteome.
SQ SEQUENCE 442 AA; 47958 MW; 75254C8D0F541CAB CRC64;

Query Match 2.0%; Score 8; DB 16; Length 442;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 LKREIEKR 257
Db 361 LKREIEKR 368

RESULT 22
Q9Y681 PRELIMINARY; PRT; 452 AA.
AC Q9Y681;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE SLAP-2 homolog.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20499367; PubMed=11042152;
RA Zhang Q.H., Ye M., Wu X.Y., Ren S.X., Zhao M., Zhao C.J., Fu G.,
RA Shen Y., Fan H.Y., Lu G., Zhong M., Xu X.R., Han Z.G., Zhang J.W.,
RA Tao J., Huang Q.H., Zhou J., Hu G.X., Gu J., Chen S.J., Chen Z.;
RT "Cloning and functional analysis of cDNAs with open reading frames for
RT 300 previously undefined genes expressed in CD34+ hematopoietic
RT stem/progenitor cells."
RL Genome Res. 10:1546-1560(2000).
DR EMBL; AF100750; AAD43014.1; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.

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DR GO; GO:0005790; C:smooth endoplasmic reticulum; TAS.
DR GO; GO:0006936; P:muscle contraction; TAS.
DR InterPro; IPR001363; Fetuin.
DR InterPro; IPR002777; PrefoldinKE2.
DR InterPro; IPR000533; Tropomyosin.
DR Pfam; PF01920; KE2; 1.
DR PRINTS; PR00194; TROPOMYOSIN.
DR PROSITE; PS01255; FETUIN_2; 1.
SQ SEQUENCE 452 AA; 52284 MW; 350581416FD23FCD CRC64;

Query Match          2.0%; Score 8; DB 4; Length 452;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 ASLOEELK 227
DB 197 ASLOEELK 204
|||||

RESULT 23
Q9M306 PRELIMINARY; PRT; 470 AA.
ID Q9M306
AC Q9M306
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN T21J18_30.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eustoids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Rieger M., Gabel C., Mueller-Auer S., Schaefer M., Zipp M.,
RA Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X., Quetier F.,
RA Salanoubat M.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Eu Arabidopsis sequencing project;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL132963; CAB87904.1; -.
DR PIR; T49272; T49272.
DR InterPro; IPR001594; Znf DHHC.
DR Pfam; PF01529; zf-DHHC_1.
DR ProDom; PD003041; Znf_DHHC; 1.
DR PROSITE; PS0216; ZF_DHHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 53086 MW; C3300B6FF397344B CRC64;

Query Match          2.0%; Score 8; DB 10; Length 470;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 DLVFLLLT 136
DB 93 DLVFLLLT 100
|||||

RESULT 24
Q28623 PRELIMINARY; PRT; 639 AA.
ID Q28623
AC Q28623
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Sarcolemmal associated protein-3.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;

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[1]
RN SEQUENCE FROM N.A.
RP Wigle J.T., Demchyshyn L., Sattar S., Pratt M., Tuana B.S.;
RA "Molecular cloning of a novel family of sarcolemmal associated coiled-
RT coil proteins; protein-protein interactions at the cell membrane.";
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U21157; AAA65597.1; -.
DR InterPro; IPR001363; Fetuin.
DR InterPro; IPR002777; PrefoldinKE2.
DR InterPro; IPR000533; Tropomyosin.
DR Pfam; PF01920; KE2; 1.
DR PRINTS; PR00194; TROPOMYOSIN.
DR PROSITE; PS01255; FETUIN_2; 1.
SQ SEQUENCE 639 AA; 73735 MW; 7511F2168A5AF671 CRC64;

Query Match          2.0%; Score 8; DB 6; Length 639;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 ASLOEELK 227
DB 413 ASLOEELK 420
|||||

RESULT 25
Q9HCH1 PRELIMINARY; PRT; 690 AA.
ID Q9HCH1
AC Q9HCH1
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein KIAA1601 (Fragment).
GN KIAA1601.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20450683; PubMed=10997877;
RA Nagase T., Kikuno R., Nakayama M., Hirosewa M., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes.
RT XVII. The complete sequences of 100 new cDNA clones from brain which
RT code for large proteins in vitro.";
RL DNA Res. 7:273-281(2000).
DR EMBL; AB046821; BAB13427.1; -.
DR Genew; HGNC:16643; SLMAP.
DR InterPro; IPR001363; Fetuin.
DR InterPro; IPR002777; PrefoldinKE2.
DR InterPro; IPR000533; Tropomyosin.
DR Pfam; PF01920; KE2; 1.
DR PRINTS; PR00194; TROPOMYOSIN.
DR PROSITE; PS01255; FETUIN_2; 1.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 690 AA; 79584 MW; 5900640A68073CF4 CRC64;

Query Match          2.0%; Score 8; DB 4; Length 690;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 ASLOEELK 227
DB 465 ASLOEELK 472
|||||

RESULT 26
Q7V419 PRELIMINARY; PRT; 892 AA.
ID Q7V419
AC Q7V419
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

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DE Alanyl-tRNA synthetase:DHHA1 domain (EC 6.1.1.7).  
GN ALAS, LOVB OR PMT2157.  
OS Prochlorococcus marinus (strain MIT 9313).  
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;  
OC Prochlorococcus;  
OX NCBI\_TaxID=74547;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22825698; PubMed=12917642;  
RA Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,  
RA Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,  
RA Johnson Z.I., Land M., Lindell D., Post A.P., Regala W., Shah M.,  
RA Shaw S.I., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,  
RA Webb E.A., Zinser E.R., Chisholm S.W.;  
RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic  
RT niche differentiation.";  
RL Nature 424:1042-1047 (2003).  
DR EMBL; BK572101; CAE2231.1; -;  
KW Aminoacyl-tRNA synthetase; Ligase; Complete proteome.  
SQ SEQUENCE 892 AA; 96492 MW; 7C87B13F8F589313 CRC64;

Query Match 2.0%; Score 8; DB 15; Length 892;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 221 SLOEELKS 228  
| | | | |  
Db 744 SLOEELKS 751

RESULT 27  
Q9LUG9 PRELIMINARY; PRT; 1309 AA.  
AC Q9LUG9;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
DE Gb|AAD13716.2.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC euroids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20277480; PubMed=10819329;  
RA Nakamura Y.;  
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence  
RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC  
RT clones.";  
RL DNA Res. 7:131-135 (2000).  
DR EMBL; AB023036; BAB02777.1; -;  
SQ SEQUENCE 1309 AA; 143093 MW; 4E85BEC186409D89 CRC64;

Query Match 2.0%; Score 8; DB 10; Length 1309;  
Best Local Similarity 100.0%; Pred. No. 82;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 164 VPLVAVNL 171  
| | | | |  
Db 404 VPLVAVNL 411

RESULT 30  
Q30A88 PRELIMINARY; PRT; 88 AA.  
AC Q30A88;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.

DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Hypothetical protein.  
GN AT3G23590/MD19 8.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC euroids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=cv. Columbia;  
RA Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,  
RA Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,  
RA Hayashizaki Y., Shinozaki K.;  
RT "Arabidopsis thaliana full-length cDNA.";  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK117119; BAC41797.1; -;  
KW Hypothetical protein.  
SQ SEQUENCE 1309 AA; 143067 MW; F569651F17C287C1 CRC64;

Query Match 2.0%; Score 8; DB 10; Length 1309;  
Best Local Similarity 100.0%; Pred. No. 82;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 164 VPLVAVNL 171  
| | | | |  
Db 404 VPLVAVNL 411

RESULT 29  
P72388 PRELIMINARY; PRT; 81 AA.  
ID P72388;  
AC P72388;  
DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE Transposase (Fragment).  
OS Staphylococcus aureus.  
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
OX NCBI\_TaxID=1280;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX TRANSPOSON=Th551;  
RA McNamara P.M., Iandolo J.J.;  
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U75367; BAB18959.1; -;  
DR InterPro; IPR002513; Transposase\_7.  
DR Pfam; PF01526; Transposase\_7; 1.  
DR NON\_TER 1  
FT NON\_TER 81  
SQ SEQUENCE 81 AA; 9490 MW; B957359583F72C12 CRC64;

Query Match 1.7%; Score 7; DB 2; Length 81;  
Best Local Similarity 100.0%; Pred. No. 77;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 SICKKVE 234  
| | | | |  
Db 4 SICKKVE 10

RESULT 30  
Q30A88 PRELIMINARY; PRT; 88 AA.  
ID Q30A88;  
AC Q30A88;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.

OX Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=622393;  
RA Op de Coul E.L.M., Coutinho R.A., van der Schoot A.,  
van Doornum G.J.J., Lukashov V.V., Goudsmit J., Cornelissen M.;  
"The impact of immigration on the env HIV-1 subtype distribution among  
heterosexuals in the Netherlands: influx of subtype B and non-B  
strains";  
RL AIDS 0:0-0(2001).  
DR EMBL; AF403886; AAL05694.1; --  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
KW AIDS; Coat protein; Glycoprotein.  
FT NON\_TER 1 1  
FT NON\_TER 88 88  
SQ SEQUENCE 88 AA; 9862 MW; D7F9DDCFCC39033 CRC64;  
  
Query Match 1.7%; Score 7; DB 15; Length 88;  
Best Local Similarity 100.0%; Pred.No. 83;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 121 LQEHFSN 127  
Db 79 LQEHFSN 85  
|||||

RESULT 31  
Q9DR26 PRELIMINARY; PRT; 88 AA.  
AC Q9DR26;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DD96061;  
RX MEDLINE=21002580; PubMed=11118076;  
RA Abebe A., Pollakis G., Fontanet A.L., Fisseha B., Tegbaru B.,  
Kliphuis A., Tesfaye G., Negassa H., Cornelissen M., Goudsmit J.,  
Rinke de Wit T.F.,  
RT "Identification of a genetic sub-cluster of HIV-1 subtype C (C')  
widespread in Ethiopia";  
RL AIDS Res. Hum. Retroviruses 16:1909-1914(2000).  
DR EMBL; AF245566; AAG40679.1; --  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
KW AIDS; Coat protein; Glycoprotein.  
FT NON\_TER 1 1  
FT NON\_TER 88 88  
SQ SEQUENCE 88 AA; 9912 MW; 7377D7552CB203B9 CRC64;  
  
Query Match 1.7%; Score 7; DB 15; Length 88;  
Best Local Similarity 100.0%; Pred.No. 83;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 121 LQEHFSN 127  
Db 79 LQEHFSN 85  
|||||

RESULT 32  
Q90BJ1 PRELIMINARY; PRT; 91 AA.  
AC Q90BJ1;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=seroconverter-B;  
RA Rinke de Wit T.F., Tsegaye A., Wolday D., Hailu B., Aklilu M.,  
Sanders E., Hagos M., Kliphuis A., Pollakis G., Krol A., Gesskus R.,  
Miedema F., Goudsmit J., Coutinho R.A., Fontanet A.L.;  
RT "Particulars of HIV-1 subtype C primary infection in Ethiopia";  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF391828; AAL06743.1; --  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
KW AIDS; Coat protein; Glycoprotein.  
FT NON\_TER 1 1  
FT NON\_TER 91 91  
SQ SEQUENCE 91 AA; 10325 MW; 81E9B71E38942BC9 CRC64;  
  
Query Match 1.7%; Score 7; DB 15; Length 91;  
Best Local Similarity 100.0%; Pred.No. 85;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 121 LQEHFSN 127  
Db 79 LQEHFSN 85  
|||||

RESULT 33  
Q9KF07 PRELIMINARY; PRT; 92 AA.  
AC Q9KF07;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Hypothetical protein BH0692.  
GN BH0692.  
OS Bacillus halodurans.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=86665;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C-125 / JCM 9153;  
RX MEDLINE=20512582; PubMed=11058132;  
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,  
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,  
Horikoshi K.;  
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus  
halodurans and genomic sequence comparison with Bacillus subtilis.";  
RL Nucleic Acids Res. 28:4317-4331(2000).  
DR EMBL; AP001509; BAB04411.1; --  
DR PIR; D83736; D83736.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 92 AA; 10704 MW; AA25939BDDC6A1B CRC64;  
  
Query Match 1.7%; Score 7; DB 16; Length 92;  
Best Local Similarity 100.0%; Pred.No. 86;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 114 ERLHKN 120  
|||||

Db 16 ERLHKN 22

RESULT 34

Q93ZJ3 PRELIMINARY; PRT; 100 AA.

AC Q93ZJ3

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE Hypothetical protein (Expressed protein) (At2g20587/At2g20587).

GN AT2G20587

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.

OX NCBI\_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,

RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,

RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,

RA Kawai J., Lam B., Lee J.M., Lin J., Liu S., Miranda M., Narusaka M.,

RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,

RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,

RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,

RA Ecker J.R.;

RT "Arabidopsis cDNA clones.";

RL Submitted (SEP-2001) to the EMBL/GenBank/DBSJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=sv. Columbia;

RA Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E.,

RA Barnstead M.E., Mason T.M., Bowman C.L., Renning C.M., Benito M.-I.,

RA Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,

RA Fraser C.M., Venter J.C.;

RL Submitted (FEB-2002) to the EMBL/GenBank/DBSJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA Haas B.J., Volfovsky N., Town C.D., Troughan M., Alexandrov N.,

RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;

RT "Full-length messenger RNA sequences greatly improve genome annotation.";

RL Genome Biol. 0:0-0(2002).

RN [4]

RP SEQUENCE FROM N.A.

RA Brover V., Troughan M., Alexandrov N., Lu Y.-P., Flavell R.,

RA Feldmann K.;

RT "Full-length cDNA from Arabidopsis thaliana.";

RL Submitted (MAR-2002) to the EMBL/GenBank/DBSJ databases.

RN [5]

RP SEQUENCE FROM N.A.

RA Kim C.J., Chen H., Cheuk R., Meyers M.C., Shinn P., Banh J.,

RA Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,

RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,

RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,

RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,

RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,

RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,

RA Ecker J.R.;

RT "Arabidopsis ORF clones.";

RL Submitted (MAY-2002) to the EMBL/GenBank/DBSJ databases.

DR EMBL; AY057495; RAL09736.1; -

DR EMBL; AC007048; RAL15363.1; -

DR EMBL; AY085547; RAL62771.1; -

DR EMBL; AY103298; RAL65350.1; -

KW Hypothetical protein.

SQ SEQUENCE 100 AA; 10451 MW; 7B12286D8FBE638B CRC64;

Query Match 1.7%; Score 7; DB 10; Length 100;

Best Local Similarity 100.0%; Pred. No. 93;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TSAVLGS 12

DB 3 TSAVLGS 9

RESULT 35

Q8NL05 PRELIMINARY; PRT; 101 AA.

AC Q8NL05

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE 30S ribosomal protein S14.

GN RPSN OR XAC0985 OR XCC0908.

OS Xanthomonas axonopodis (pv. citri), and

OS Xanthomonas campestris (pv. campestris).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;

OC Xanthomonadaceae; Xanthomonas.

OX NCBI\_TaxID=92829, 340;

RN [1]

RP SEQUENCE FROM N.A.

RC SPECIES=X.a.citri, and X.c.campestris;

RC STRAIN=306 / ATCC 13302 / XV 101, and ATCC 33913 / NCPPB 528;

RC MEDLINE=22022145, PubMed=12024217;

RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,

RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RA Setubal J.C., Kitajima J.P.;

RT "Comparison of the genomes of two Xanthomonas pathogens with differing host specificities.";

RL Nature 417:459-463(2002).

DR EMBL; AB011728; RAL35868.1; -

DR EMBL; AB012189; RAL40218.1; -

DR GO; GO:0005622; C:intracellular; IEA.

DR GO; GO:0005840; C:ribosome; IEA.

DR GO; GO:0003735; P:protein biosynthesis; IEA.

DR GO; GO:0006412; P:ribosome biogenesis; IEA.

DR InterPro: IPR001209; Ribosomal S14.

DR Pfam: PF00253; Ribosomal S14; i.

KW Ribosomal protein; Complete proteome.

SQ SEQUENCE 101 AA; 11499 MW; 9ECC54DE080CF5A CRC64;

Query Match 1.7%; Score 7; DB 16; Length 101;

Best Local Similarity 100.0%; Pred. No. 94;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 ALKKILS 90

DB 26 ALKKILS 32

RESULT 36

Q9LTQ1 PRELIMINARY; PRT; 103 AA.

AC Q9LTQ1

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)

DE Emb|CAB39646.1.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

eurosid II; Brassicales; Brassicaceae; Arabidopsis.  
OK NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Columbia;  
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;  
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Columbia;  
RX MEDLINE=20277480; PubMed=10819329;  
RA Nakamura Y.;  
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence  
RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC  
RT clones.";  
RL DNA Res. 7:131-135(2000).  
DR EMBL; AB024036; BAB02823.1; -;  
SQ SEQUENCE 103 AA; 11741 MW; B66684E4B801FD92 CRC64;  
  
Query Match 1.7%; Score 7; DB 10; Length 103;  
Best Local Similarity 100.0%; Pred.No. 95;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 206 DGSLEKEV 212  
Db |||||  
72 DGSLEKEV 78  
  
RESULT 37  
Q82IX9 PRELIMINARY; PRT; 104 AA.  
AC Q82IX9;  
DT 01-MAR-2002 (TRENBLrel. 20, Created)  
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)  
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
DE Putative chaperrone.  
GN SUGO OR YPO0355.  
OS Yersinia pestis.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Yersinia.  
OX NCBI\_TaxID=632;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CO-92 / Biovar Orientalis;  
RX MEDLINE=21470413; PubMed=11586360;  
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,  
RA Prentice W.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,  
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,  
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,  
RA Feltwell T., Hamlin N., Holroyd S., Jagsels K., Karlyshev A.V.,  
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,  
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;  
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";  
RL Nature 413:523-527(2001).  
DR EMBL; AJ414142; CAC89214.1; -;  
DR PIR; AC0044; AC0044.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR InterPro; IPR000390; Smr.  
DR Pfam; PF00893; Multi Drug Res; 1.  
DR Hypothetical protein; Complete proteome.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 104 AA; 10651 MW; 5DADB41E0B97B5B8 CRC64;  
  
Query Match 1.7%; Score 7; DB 16; Length 104;  
Best Local Similarity 100.0%; Pred.No. 96;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 135 LTPSIIT 141  
Db |||||  
29 LTPSIIT 35  
  
RESULT 38  
Q8XGT8 PRELIMINARY; PRT; 105 AA.  
AC Q8XGT8;  
DT 01-MAR-2002 (TRENBLrel. 20, Created)  
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)  
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
DE SUGO protein (Putative DMT superfamily transport protein).  
GN SUGO OR T4390 OR STM4338 OR STY4699.  
OS Salmonella typhi, and  
OS Salmonella typhimurium.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Salmonella.  
OX NCBI\_TaxID=601, 602;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931;  
RX MEDLINE=22531367; PubMed=12644504;  
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,  
RA Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;  
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2  
RT and CT18.";  
RL J. Bacteriol. 185:2330-2337(2003).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;  
RX MEDLINE=21534948; PubMed=11677609;  
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,  
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,  
RA Leonard S., Nguyen C., Scott K., Holmes A., Hien T.T., Holroyd S., Jagsels K.,  
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,  
RA Waterston R., Wilson R.K.;  
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium  
RT LT2.";  
RL Nature 413:852-856(2001).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC SPECIES=S.typhi; STRAIN=CT18;  
RX MEDLINE=21534947; PubMed=11677608;  
RA Parkhill J., Dougan G., James K.D., Bentley S.D., Holden M.T.G., Sebahia M.,  
RA Churcher C., Mungall K.L., Brooks K., Chillingworth T., Conerton P.,  
RA Baker S., Basham D., Brooks K., Davies R.M., Dowd L., White N., Farrar J.,  
RA Cronin A., Davis P., Davies R.M., Dougan G., Chillingworth T.,  
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagsels K.,  
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,  
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,  
RA Whitehead S., Barrell B.G.;  
RT "Complete genome sequence of a multiple drug resistant Salmonella  
RT enterica serovar Typhi CT18.";  
RL Nature 413:848-852(2001).  
DR EMBL; AE016849; AA071841.1; -;  
DR EMBL; AE008903; AAL23161.1; -;  
DR EMBL; AL627283; CAD06818.1; -;  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR InterPro; IPR000390; Smr.  
DR Pfam; PF00893; Multi Drug Res; 1.  
DR Hypothetical protein; Complete proteome.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 105 AA; 10869 MW; 1D396AF413953701 CRC64;  
  
Query Match 1.7%; Score 7; DB 16; Length 105;  
Best Local Similarity 100.0%; Pred.No. 97;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 135 LTPSIIT 141  
Db |||||  
29 LTPSIIT 35  
  
RESULT 39  
Q9LWQ0 PRELIMINARY; PRT; 108 AA.  
AC Q9LWQ0;  
DT 01-OCT-2000 (TRENBLrel. 15, Created)  
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)  
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)

DE EST AU065411(R3610) corresponds to a region of the predicted gene  
DN (P0489A05.29 protein).  
GN P0489A05.29.  
OS Oryza sativa (Rice).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzaceae; Oryza.  
OX NCBI\_TaxID=4530;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Nipponbare;  
RA Sasaki T.; Matsumoto T.; Yamamoto K.;  
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC  
clone:P0489A05.29";  
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AP001551; BAA32945.1; -;  
DR EMBL; AP003105; BAA33006.1; -;  
DR Gramene; Q9LWQ0; -;  
SQ SEQUENCE 108 AA; 10846 MW; 1768BA3625B367D0 CRC64;  
  
Query Match 1.7%; Score 7; DB 10; Length 108;  
Best Local Similarity 100.0%; Pred. No. 99;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 130 LVFLLLT 136  
DB 13 LVFLLLT 19  
  
RESULT 40  
Q8E6E9 PRELIMINARY; PRT; 110 AA.  
AC Q8E6E9;  
DT 01-WAR-2003 (TrEMBLrel. 23, Created)  
DT 01-WAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Hypothetical protein.  
GN GBS0619.  
OS Streptococcus agalactiae (serotype III).  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
OC Streptococcus  
OX NCBI\_TaxID=216495;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MEM316 / Serotype III;  
RX MEDLINE=224242508; PubMed=12354221;  
RA Glaser P., Rusnick C., Buchrieser C., Chevalier F., Frangeul L.,  
RA Msadek T., Zouine M., Couve E., Lalicui L., Poyart C., Trieu-Cuot P.,  
RA Kunst F.;  
RT "Genome sequence of Streptococcus agalactiae, a pathogen causing  
RT invasive neonatal disease.";  
RL Mol. Microbiol. 45:1499-1513 (2002).  
DR EMBL; AL766846; CAD46263.1; -;  
DR Sgallist; gbs0619; -;  
DR GO; GO:0016020; C:membrane; IEA.  
DR InterPro; IPR005877; Gpos\_Ysirk.  
DR Pfam; PF04650; Ysirk\_signal; 1.  
DR TIGRFAMs; TIGR01168; Ysirk\_signal; 1.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 110 AA; 11790 MW; A646631D04201ADF CRC64;  
  
Query Match 1.7%; Score 7; DB 16; Length 110;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 STSAVLS 11

Db 84 STSAVLS 90  
|||||  
RESULT 41  
Q8A302 PRELIMINARY; PRT; 114 AA.  
AC Q8A302;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
GN BT3153  
OS Bacteroides thetaiotaomicron.  
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;  
OC Bacteroidaceae; Bacteroides.  
OX NCBI\_TaxID=818;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=VPI-5482 / ATCC 29148;  
RX MEDLINE=22550858; PubMed=12663928;  
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,  
RA Chiang H.C., Hooper L.V., Gordon J.I.;  
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";  
RL Science 299:2074-2076 (2003).  
DR EMBL; AE016939; AAO78259.1; -;  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR InterPro; IPR001387; HTH\_3.  
DR Pfam; PF01381; HTH\_3; 1.  
DR SMART; SM00530; HTH\_XRE; 1.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 114 AA; 13497 MW; 1D123D55E0F9EF18 CRC64;  
  
Query Match 1.7%; Score 7; DB 16; Length 114;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 245 KDVNRLK 251  
DB 47 KDVNRLK 53  
|||||  
RESULT 42  
Q7ZEP5 PRELIMINARY; PRT; 115 AA.  
AC Q7ZEP5;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein (fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=02timene1019;  
RA Subtuent K.;  
RT "Molecular Epidemiology of HIV-1 in Thailand.";  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY248086; AAP14146.1; -;  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR InterPro; IPR000777; GP120.  
KW Envelope protein.  
FT NON\_TER 1  
FT NON\_TER 115  
SQ SEQUENCE 115 AA; 13100 MW; 1188484FA395449B CRC64;  
  
Query Match 1.7%; Score 7; DB 15; Length 115;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 121 LQEHFSN 127

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DB 73 LQEHFSN 79
|||||
RESULT 43
Q8V6V7 PRELIMINARY; PRT; 116 AA.
AC Q8V6V7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Halovirus HF2.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
OX NCBI_TaxID=33771;
RN [1]
RP SEQUENCE FROM N.A.
RA Tang S.-L., Fisher C., Ngui K., Nuttall S.D., Dyal-Smith M.L.;
RT "Sequence and transcription of halovirus HF2.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF222060; AAL54923.1; -.
KW Hypothetical protein.
SQ SEQUENCE 116 AA; 13646 MW; EA69EC3F77FFA37A CRC64;

Query Match 1.7%; Score 7; DB 12; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 390 TDEIEK 396
|||||
DB 88 TDEIEK 94

RESULT 44
Q7TDP0 PRELIMINARY; PRT; 116 AA.
AC Q7TDP0;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Halovirus HF1.
OC Viruses; unclassified viruses; Haloviruses.
OX NCBI_TaxID=222645;
RN [1]
RP SEQUENCE FROM N.A.
RA Tang S.-L., Nuttall S.D., Dyal-Smith M.L.;
RT "Nucleotide sequence of halovirus HF1: close similarity to HF2 and evidence for a recent and large recombination event.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY190604; AAO61301.1; -.
KW Hypothetical protein.
SQ SEQUENCE 116 AA; 13646 MW; EA69EC3F77FFA37A CRC64;

Query Match 1.7%; Score 7; DB 12; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 390 TDEIEK 396
|||||
DB 88 TDEIEK 94

RESULT 45
Q8Y4K1 PRELIMINARY; PRT; 136 AA.
AC Q8Y4K1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein lmo2437.
GN LMO2437.
OS Listeria monocytogenes.
```

```
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EGD-e / Serovar 1/2a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaser F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Baquero F., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Charbit A., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Domann E., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Entian K.-D., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Gautier L., Kaerst U., Kretz J., Kuhn M., Kunst F., Kurapkak G.,
RA Jones L.-M., Matounam A., Mata Vicente J., Ng E., Nedjari H.,
RA Madueno E., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Madsen B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA Remmel B., Voss H., Weiland J., Cossart P.;
RA Vazquez-Boland J.-A., Voss H., Weiland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
DR EMBL; AL591983; CAD00515.1; -.
DR PIR; A81379; A81379.
DR Listlist; LMO02437; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 136 AA; 15676 MW; 75B479CEA21F889B CRC64;

Query Match 1.7%; Score 7; DB 16; Length 136;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 238 QAVDKLV 244
|||||
DB 86 QAVDKLV 92

RESULT 46
Q9UZRS PRELIMINARY; PRT; 136 AA.
AC Q9UZRS;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein PYRAB10800.
GN PYRAB10800 OR PAB0720.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OX NCBI_TaxID=29292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GE5 / Orsay;
RA Heilig R.;
RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure and evolution.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ248286; CAB49991.1; -.
DR PIR; B75086; B75086.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 136 AA; 15404 MW; 6920B94FD72B6917 CRC64;

Query Match 1.7%; Score 7; DB 17; Length 136;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 392 EEIEKMK 398
|||||
DB 98 EEIEKMK 104

RESULT 47
Q8UIN2 PRELIMINARY; PRT; 137 AA.
AC Q8UIN2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
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DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
GN Hypothetical protein PF1174.
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome.";
RL Submitted (FEB-2002) to the ENBL/GenBank/DBJ databases.
DR EMBL; AF010226; AAL51298.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 137 AA; 15687 MW; 4EFC98EA2E986FD1 CRC64;

Query Match 1.7%; Score 7; DB 17; Length 137;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 392 REIERMK 398
Db 98 REIERMK 104
|||||

RESULT 48
ID Q93MB9 PRELIMINARY; PRT; 138 AA.
AC Q93MB9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein PCP28.
GN PCP28.
OS Clostridium perfringens.
OG Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13 / Type A;
RX MEDLINE=21664373; PubMed=11792842;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater."
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR EMBL; AF003515; BAB2466.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR InterPro; IPR005357; UPF0150.
DR Pfam; PF03681; UPF0150; 1.
KW Plasmid; Hypothetical protein; Complete proteome.
SQ SEQUENCE 138 AA; 15675 MW; 64B4C0FA6ED901E2 CRC64;

Query Match 1.7%; Score 7; DB 16; Length 138;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 389 ETDEEIE 395
Db 56 ETDEEIE 62
|||||

RESULT 49
ID Q9XX55 PRELIMINARY; PRT; 140 AA.
AC Q9XX55;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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```
DE Y38H6C.3 protein.
GN Y38H6C.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA White S.;
RL Submitted (SEP-1998) to the ENBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C. elegans: A platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; AL031630; CAA20983.1; -.
DR FIR; T26693; T26693.
DR WormPep; Y38H6C.3; CE19097.
SQ SEQUENCE 140 AA; 16445 MW; AEDC919D930D6B58 CRC64;

Query Match 1.7%; Score 7; DB 5; Length 140;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 252 REIEKER 258
Db 44 REIEKER 50
|||||

RESULT 50
ID Q93SS4 PRELIMINARY; PRT; 143 AA.
AC Q93SS4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Exbd.
GN Exbd.
OS Plesiomonas shigelloides (Aeromonas shigelloides).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Plesiomonas.
OX NCBI_TaxID=703;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21189295; PubMed=11292789;
RA Henderson D.P., Wyckoff E.E., Rashidi C.E., Verlei H., Oldham A.L.;
RT "Characterization of the Plesiomonas shigelloides genes encoding the
RT Heme Iron Utilization System."
RL J. Bacteriol. 183:2715-2723(2001).
DR EMBL; AY008342; AAG23398.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003400; Exbd.
DR Pfam; PF02472; Exbd; 1.
SQ SEQUENCE 143 AA; 15711 MW; E713E9FFFD1088A CRC64;

Query Match 1.7%; Score 7; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 LVFLLLT 136
Db 28 LVFLLLT 34
|||||

RESULT 51
ID Q89F14 PRELIMINARY; PRT; 144 AA.
AC Q89F14;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
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DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DE 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE BLR6887 protein.
GN BLR6887.
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA 110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Ideawa K., Iriguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110."
RL DNA Res. 9:189-197(2002).
DR EMBL; AP005960; BAC52152.1; -.
KW Complete proteome.
SQ SEQUENCE 144 AA; 15281 MW; 924ABDEBF76679F8 CRC64;

Query Match 1.7%; Score 7; DB 16; Length 144;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 189 TGFSRAV 195
DB 28 TGFSRAV 34
|||||

RESULT 52
Q8EB62 PRELIMINARY; PRT; 145 AA.
ID Q8EB62
AC Q8EB62;
RX MEDLINE=22297686; PubMed=12368813;
RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,
RA Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,
RA Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,
RA Vanatavan J., Weidman J., Imprial M., Lee K., Berry K., Lee C.,
RA Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,
RA Feldblyum T.V., Smith H.O., Venter J.C., Neallson K.H., Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis."
RT Nat. Biotechnol. 20:1118-1123(2002).
DR EMBL; AE015802; AAN56657.1; -.
DR TIGR; SO3672; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003400; Exbd.
DR Pfam; PF02472; Exbd; 1.
KW Complete proteome.
SQ SEQUENCE 145 AA; 15477 MW; 7920728490CF7219 CRC64;

Query Match 1.7%; Score 7; DB 16; Length 145;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 DLVFLLL 135
DB 97 DLVFLLL 103
|||||

RESULT 54
Q8UIG7 PRELIMINARY; PRT; 153 AA.
ID Q8UIG7
AC Q8UIG7;
RX MEDLINE=21608551; PubMed=11743193;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Chura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutayin T., Levy R., Li M.-J., McClelland E., Palmeri A., Gordon D.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58."
RT Science 294:2317-2323(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Mullin L.,
RA Qurollo B., Goldman B.S., Gao Y., Askenazi M., Halling C., Mullin L.,
RA Houmlel K., Gordon J., Vaudin M., Doughty D., Iartchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gursion J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58."
RT Science 294:2323-2328(2001).
RL EMBL; AE009004; AAL4352.1; -.
DR EMBL; AE007971; AAK86147.1; -.
DR PIR; AB2617; AB2617.
DR PIR; B97399; B97399.
DR GO; GO:0005351; F:sugar porter activity; IEA.
DR GO; GO:0009401; P:phosphoenolpyruvate-dependent sugar phospho. . .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006320; PtsN_nitro_regn.
DR InterPro; IPR002178; Pts_EIIA_2.
DR Pfam; PF00359; Pts_EIIA_2; 1.
DR ProDom; PD001689; Pts_EIIA_2; 1.
DR TIGRPFAMs; TIGR01419; nitro_reg_IIA; 1.
DR PROSITE; PS00372; Pts_EIIA_2; 1.
KW Complete proteome.
SQ SEQUENCE 153 AA; 16470 MW; EF28EE87ADA99450 CRC64;

Query Match 1.7%; Score 7; DB 16; Length 153;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 DLVFLLL 135
DB 97 DLVFLLL 103
|||||

RESULT 54
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Q8D1E4
ID Q8D1E4 PRELIMINARY; PRT; 153 AA.
AC Q8D1E4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-OCT-2001 (TrEMBLrel. 23, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Suppresses groEL, may be chaparone.
SUGS SUGS OR Y0613.
OS Versinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KIM5 / Biovar Mediaevalis;
RC MEDLINE=22137863; PubMed=12142430;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM.";
RL J. Bacteriol. 184:4601-4611(2002).
DR EMBL; AE013663; AAM84201.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR000390; Smr.
DR Pfam; PF00893; Multi_Drug_Res; 1.
SQ SEQUENCE 153 AA; 16153 MW; FFE92A5044FBF195 CRC64;

Query Match 1.7%; Score 7; DB 16; Length 153;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 135 LTPSIIT 141
    |||||
DB 78 LTPSIIT 84

RESULT 55
Q98GS7 PRELIMINARY; PRT; 154 AA.
AC Q98GS7;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Phosphotransferase system enzyme II (EC 2.7.1.69).
GN MLL3194.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF301099;
RC MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idekawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumoto A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AF003001; BAB50139.1; -
DR GO; GO:0008982; F:sugar porter activity; IEA.
DR GO; GO:0005351; F:transferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0008401; P:phosphoenolpyruvate-dependent sugar phospho. . .; IEA.
DR GO; GO:0008810; P:transport; IEA.
DR InterPro; IPR006320; PtsN nitro. regn.
DR InterPro; IPR002178; Pts_EIIA_2.
DR Pfam; PF00359; Pts_EIIA_2; 1.
DR ProDom; PD001689; Pts_EIIA_2; 1.

Q98GS7 PRELIMINARY; PRT; 154 AA.
AC Q98GS7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Probable nitrogen regulatory IIA protein (EC 2.7.1.69).
GN PtsN OR R00379 OR SMC01141.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RC MEDLINE=21396507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA Pohl T., Portetelie D., Puhler A., Purnelle B., Ramsperger U.,
RA Renard C., Thebault P., Vandenbol M., Weidner S., Gallibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
DR EMBL; AL591783; CAC41816.1; -
DR GO; GO:0008982; F:protein-N(Pi)-phosphohistidine-sugar phospho. . .; IEA.
DR GO; GO:0005351; F:sugar porter activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0008401; P:phosphoenolpyruvate-dependent sugar phospho. . .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006320; PtsN nitro. regn.
DR InterPro; IPR002178; Pts_EIIA_2.
DR Pfam; PF00359; Pts_EIIA_2; 1.
DR ProDom; PD001689; Pts_EIIA_2; 1.
DR TIGRFAMs; TIGR01419; nitro_reg_IIA; 1.
DR PROSITE; PS00372; Pts_EIIA_2; 1.
KW Transferase; Complete proteome.
SQ SEQUENCE 154 AA; 16438 MW; 79EBE44F78BE9462 CRC64;

Query Match 1.7%; Score 7; DB 16; Length 154;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 DLVFLLL 135
    |||||
DB 97 DLVFLLL 103

RESULT 57
Q8YEUI PRELIMINARY; PRT; 154 AA.
AC Q8YEUI;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Nitrogen regulatory IIA protein (EC 2.7.1.69).
GN BME1786.
OS Brucella melitensis.
```

```
DR TIGRFAMs; TIGR01419; nitro_reg_IIA; 1.
DR PROSITE; PS00372; Pts_EIIA_2; 1.
KW Transferase; Complete proteome.
SQ SEQUENCE 154 AA; 16302 MW; AE8B5B5EB30301EC CRC64;

Query Match 1.7%; Score 7; DB 16; Length 154;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 DLVFLLL 135
    |||||
DB 97 DLVFLLL 103

RESULT 56
Q92SJ9 PRELIMINARY; PRT; 154 AA.
AC Q92SJ9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Probable nitrogen regulatory IIA protein (EC 2.7.1.69).
GN PtsN OR R00379 OR SMC01141.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RC MEDLINE=21396507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA Pohl T., Portetelie D., Puhler A., Purnelle B., Ramsperger U.,
RA Renard C., Thebault P., Vandenbol M., Weidner S., Gallibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
DR EMBL; AL591783; CAC41816.1; -
DR GO; GO:0008982; F:protein-N(Pi)-phosphohistidine-sugar phospho. . .; IEA.
DR GO; GO:0005351; F:sugar porter activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0008401; P:phosphoenolpyruvate-dependent sugar phospho. . .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006320; PtsN nitro. regn.
DR InterPro; IPR002178; Pts_EIIA_2.
DR Pfam; PF00359; Pts_EIIA_2; 1.
DR ProDom; PD001689; Pts_EIIA_2; 1.
DR TIGRFAMs; TIGR01419; nitro_reg_IIA; 1.
DR PROSITE; PS00372; Pts_EIIA_2; 1.
KW Transferase; Complete proteome.
SQ SEQUENCE 154 AA; 16438 MW; 79EBE44F78BE9462 CRC64;

Query Match 1.7%; Score 7; DB 16; Length 154;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 DLVFLLL 135
    |||||
DB 97 DLVFLLL 103

RESULT 57
Q8YEUI PRELIMINARY; PRT; 154 AA.
AC Q8YEUI;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Nitrogen regulatory IIA protein (EC 2.7.1.69).
GN BME1786.
OS Brucella melitensis.
```

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Brucellaceae; Brucella.  
OX NCBI\_TaxID=29459;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=16M / ATCC 23456 / Biotype 1;  
RX MEDLINE=20020109; PubMed=11756688;  
RA DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mijer C., Los T.,  
RA Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,  
RA Jablonowski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltzman E.,  
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,  
RA Haselkorn R., Kyprides N., Overbeek R.;  
RT "The genome sequence of the facultative intracellular pathogen  
Brucella melitensis";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).  
DR EMBL; AE009611; AAL52967.1; -;  
DR PIR; AD3475; AD3475;  
DR GO; GO:0008982; F:protein-N(P)-phosphohistidine-sugar phosph. . . ; IEA.  
DR GO; GO:0005351; F:sugar porter activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0009401; F:phosphoenolpyruvate-dependent sugar phospho. . . ; IEA.  
DR GO; GO:0006810; F:transport; IEA.  
DR InterPro; IPR006320; P:snr protein.  
DR InterPro; IPR002178; P:snr protein.  
DR Pfam; PF00359; PTS\_EIIA\_2; 1.  
DR ProDom; PD001689; PTS\_EIIA\_2; 1.  
DR TIGRPFAMs; TIGR01419; nitro\_reg\_IIA; 1.  
DR PROSITE; PS00372; PTS\_EIIA\_2; 1.  
KW Transferase; Complete proteome.  
SQ SEQUENCE 154 AA; 16497 MW; D53523086D684FB4 CRC64;

Query Match 1.7%; Score 7; DB 16; Length 154;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 DLVFLLL 135  
Db 97 DLVFLLL 103

RESULT 58  
Q8G226 PRELIMINARY; PRT; 154 AA.  
AC Q8G226;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DE PTS system, nitrogen regulatory IIA component.  
GN PTSN OR BR0161.  
OS Brucella suis.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Brucellaceae; Brucella.  
OX NCBI\_TaxID=29461;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1330 / Biovar 1;  
RX Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,  
RA Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,  
RA Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,  
RA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,  
RA Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,  
RA Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;  
RT "The Brucella suis genome reveals fundamental similarities between  
animal and plant pathogens and symbionts";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153 (2002).  
DR EMBL; AE014330; AAN29114.1; -;  
DR TIGR; BR0161; -;  
DR GO; GO:0005351; F:sugar porter activity; IEA.  
DR GO; GO:0009401; F:phosphoenolpyruvate-dependent sugar phospho. . . ; IEA.  
DR GO; GO:0006810; F:transport; IEA.  
DR InterPro; IPR006320; P:snr protein.  
DR InterPro; IPR002178; P:snr protein.

DR Pfam; PF00359; PTS\_EIIA\_2; 1.  
DR ProDom; PD001689; PTS\_EIIA\_2; 1.  
DR TIGRPFAMs; TIGR01419; nitro\_reg\_IIA; 1.  
RW PROSITE; PS00372; PTS\_EIIA\_2; 1.  
KW Complete proteome.  
SQ SEQUENCE 154 AA; 16467 MW; DFES30086D685CB4 CRC64;

Query Match 1.7%; Score 7; DB 16; Length 154;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 DLVFLLL 135  
Db 97 DLVFLLL 103

RESULT 59  
Q9AKF2 PRELIMINARY; PRT; 155 AA.  
AC Q9AKF2;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Rickettsia rickettsii.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;  
OC Rickettsiaceae; Rickettsiae; Rickettsia.  
OX NCBI\_TaxID=783;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=84-21C;  
RX MEDLINE=21219194; PubMed=11319266;  
RA Andersson J.O., Andersson S.G.E.;  
RT "Pseudogenes, junk DNA and the dynamics of Rickettsia genomes.";  
RL Mol. Biol. Evol. 18:829-839 (2001).  
DR EMBL; AJ293329; CAC33713.1; -;  
KW Hypothetical protein.  
SQ SEQUENCE 155 AA; 17335 MW; C7FC8DC4948E288B CRC64;

Query Match 1.7%; Score 7; DB 2; Length 155;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 LLTTPSI 139  
Db 14 LLTTPSI 20

RESULT 60  
Q9LIZ1 PRELIMINARY; PRT; 156 AA.  
AC Q9LIZ1;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DE Hypothetical protein.  
OS Oryza sativa (Rice).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzaceae; Oryza.  
OX NCBI\_TaxID=4530;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Nipponbare;  
RA Sasaki T., Matsumoto T., Yamamoto K.;  
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC  
clone:PO693E08";  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AP001081; BAA90382.1; -;  
DR Gramene; Q9LIZ1; -;  
KW Hypothetical protein.  
SQ SEQUENCE 156 AA; 16354 MW; CE094FAE763290EE CRC64;

```
Query Match 1.7%; Score 7; DB 10; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 STGFSRA 194
DB 98 STGFSRA 104

RESULT 61
Q9RN96 PRELIMINARY; PRT; 158 AA.
AC Q9RN96;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 22, Last annotation update)
DE M protein precursor (Fragment).
GN EMM.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Iactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NS292;
RA Bessen D.E.; Carapetis J.R.; Beall B.; Katz R.; Hibble M.;
RA Currie B.J.; Collingridge T.; Izzo M.W.; Scaramuzzino D.A.;
RA Sriprakash K.S.;
RT "Contrasting Molecular Epidemiology of Group A Streptococci Causing
RT Tropical and Non-Tropical Infections.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RW EMBL; AF193966; AAD55745.1; --
KW Signal
FT NON_TER 1 1
FT SIGNAL <1 22 POTENTIAL.
FT CHAIN 23 >158 M PROTEIN.
FT NON_TER 158 158
FT SEQUENCE 158 AA; 17948 MW; 7C2193A1DF6FE51C CRC64;

Query Match 1.7%; Score 7; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 KREIEKR 257
DB 148 KREIEKR 154

RESULT 62
Q94UY8 PRELIMINARY; PRT; 173 AA.
AC Q94UY8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE NADH dehydrogenase subunit 6.
OS Pluvialis squatarola (Black-bellied plover).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Charadriiformes; Charadriidae;
OC Pluvialis.
OX NCBI_TaxID=171273;
RN [1]
RP SEQUENCE FROM N.A.
RC Chen X.-F.; Li Q.-W.;
RA "Studies on the phylogenetic relationship among 14 species of
RT Charadriiformes from the complete mitochondrial NADH dehydrogenase
RT subunit 6 (ND6) gene.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RW EMBL; AF411399; AAL29218.1; --
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
DR GO; GO:0006120; P:mitochondrial electron transport, NADH to u. . .; IEA.
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DR InterPro; IPR001457; Oxidored_q3.
DR Pfam; PF00499; oxidored_q3; 1.
KW Mitochondrion.
SQ SEQUENCE 173 AA; 18073 MW; 7E35C3692D8E7D31 CRC64;

Query Match 1.7%; Score 7; DB 8; Length 173;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 FVLGALA 19
DB 12 FVLGALA 18

RESULT 63
Q958D2 PRELIMINARY; PRT; 173 AA.
ID Q958D2;
AC Q958D2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE NADH dehydrogenase subunit VI.
OS Tinamus major (Great tinamou).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Palaeognathae; Tinamiformes; Tinamidae; Tinamus.
OX NCBI_TaxID=30468;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21263106; PubMed=11370967;
RA Haddrath O.; Baker A.J.;
RT "Complete mitochondrial DNA genome sequences of extinct birds: ratite
RT phylogenetics and the vicariance biogeography hypothesis.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 268:939-945(2001).
DR EMBL; AF338707; AAK53254.1; --
DR PIR; E90621; E90621.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
DR GO; GO:0006120; P:mitochondrial electron transport, NADH to u. . .; IEA.
DR InterPro; IPR001457; Oxidored_q3.
DR Pfam; PF00499; oxidored_q3; 1.
KW Mitochondrion.
SQ SEQUENCE 173 AA; 18293 MW; D56C94812DD14F4A CRC64;

Query Match 1.7%; Score 7; DB 8; Length 173;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 FVLGALA 19
DB 12 FVLGALA 18

RESULT 64
Q958A8 PRELIMINARY; PRT; 174 AA.
ID Q958A8;
AC Q958A8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE NADH dehydrogenase subunit VI.
OS Pterocnemia pennata (Lesser rhea) (Darwin's rhea).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Palaeognathae; Rheiformes; Rheidae; Pterocnemia.
OX NCBI_TaxID=8795;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21263106; PubMed=11370967;
RA Haddrath O.; Baker A.J.;
RT "Complete mitochondrial DNA genome sequences of extinct birds: ratite
RT phylogenetics and the vicariance biogeography hypothesis.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 268:939-945(2001).
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RN  SEQUENCE FROM N.A.
RP  Haddath O., Baker A.J.;
RA  Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RL  EMBL; AF338709; AAK53280.1; -.
DR  PIR; E90617; E90617.
DR  GO; GO:0005739; C:mitochondrion; IEA.
DR  GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
DR  GO; GO:0006120; P:mitochondrial electron transport, NADH to u. . .; IEA.
DR  InterPro; IPR001457; Oxidored_g3.
DR  Pfam; PF00499; Oxidored_g3; 1.
KW  Mitochondrion.
SQ  SEQUENCE 174 AA; 18296 MW; 51B6C82E6CA22746 CRC64;

Query Match 1.7%; Score 7; DB 8; Length 174;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 FVLGALA 19
DB 13 FVLGALA 19
|||||

RESULT 65
O57255 PRELIMINARY; PRT; 177 AA.
AC O57255;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative 20.7k protein.
GN MVAL75R.
OS Vaccinia virus (strain Ankara).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=126794;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ankara;
RA Antoine G., Scheiflinger F., Falkner F.G., Dörner F.;
RT "The complete genomic sequence of the Modified Vaccinia Ankara (MVA) strain.";
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U94848; AAB96549.1; -.
DR PIR; T37444; T37444.
SQ SEQUENCE 177 AA; 20732 MW; 5033B53EB73979E6 CRC64;

Query Match 1.7%; Score 7; DB 12; Length 177;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 SIITESC 144
DB 62 SIITESC 68
|||||

RESULT 66
O8QMP4 PRELIMINARY; PRT; 181 AA.
AC O8QMP4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE V192.
OS Cowpox virus (CPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10243;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Brighton Red;
RX MEDLINE=83117629; PubMed=6961398;
RX Pickup D.J., Bastia D., Stone H.O., Joklik W.K.;

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RT "Sequence of terminal regions of cowpox virus DNA: arrangement of
RT repeated and unique sequence elements.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:7112-7116(1982).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Brighton Red;
RX MEDLINE=90177240; PubMed=2309453;
RA Parsons B.L., Pickup D.J.;
RT "Transcription of Orthopoxvirus telomeres at late times during
RT infection.";
RL Virology 175:69-80(1990).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Brighton Red;
RX MEDLINE=91196263; PubMed=2014645;
RA Hu F.Q., Pickup D.J.;
RT "Transcription of the terminal loop region of vaccinia virus DNA is
RT initiated from the telomere sequences directing DNA resolution.";
RL Virology 181:716-720(1991).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Brighton Red;
RX MEDLINE=94378510; PubMed=8091665;
RA Hu F.Q., Smith C.A., Pickup D.J.;
RT "Cowpox virus contains two copies of an early gene encoding a soluble
RT secreted form of the type II TNF receptor.";
RL Virology 204:343-356(1994).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Brighton Red;
RA Pickup D.J.;
RL Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=Brighton Red;
RA Dietrich F.S., Ray C.A., Sharma A.D., Allen A., Pickup D.J.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF482758; AAM13640.1; -.
SQ SEQUENCE 181 AA; 21169 MW; 35E8A36E26A89D45 CRC64;

Query Match 1.7%; Score 7; DB 12; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 SIITESC 144
DB 61 SIITESC 67
|||||

RESULT 67
O9JFT2 PRELIMINARY; PRT; 181 AA.
AC O9JFT2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE C3R.
OS Ectromelia virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=12643;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Moscow;
RX MEDLINE=20192152; PubMed=10725549;
RX Chen N., Buller R.M.L., Wall E.M., Upton C.;
RT "Analysis of host response modifier ORFs of ectromelia virus, the
RT causative agent of mousepox.";
RL Virus Res. 66:155-173(2000).
DR EMBL; AF012825; AAC9562.1; -.
SQ SEQUENCE 181 AA; 21184 MW; 727E5DC1B1D8C927 CRC64;

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Query Match 1.7%; Score 7; DB 12; Length 181;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 SIITESC 144  
Db 61 SIITESC 67

RESULT 68  
ID Q8BX5 PRELIMINARY; PRT; 181 AA.  
AC Q8BX5;  
DT 01-JUN-2002 (T-EMBLrel. 21, Created)  
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)  
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)  
DE Predicted phosphoesterase.  
GN TTE0681.  
OS Thermoanaerobacter tengcongensis.  
OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;  
OC Thermoanaerobacteriaceae; Thermoanaerobacter.  
OX NCBI\_TaxID=119072;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MB4 / JCM 11007;  
RX MEDLINE=2192816; PubMed=1197336;  
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,  
Tan H., Xue Y., Xu Y., Lai X., Huang H., Dong X., Ma Y., Ling L.,  
Chen Y., Chen R., Wang J., Yu J., Yang H.;  
RT "A complete sequence of T. tengcongensis genome.";  
RL Genome Res. 12:689-700(2002).  
DR EMBL; AS013036; AAM23945.1; -;  
DR GO; GO:0016787; F.hydrolase activity; IEA.  
DR InterPro; IPR004843; M-dpstrase.  
DR InterPro; IPR000979; UPF0025.  
DR Pfam; PF00149; Metallophos; 1.  
DR TIGRFAMs; TIGR00040; yfcs; 1.  
KW Complete proteome.  
SQ SEQUENCE 181 AA; 20412 MW; DE45021A081FED6D CRC64;

Query Match 1.7%; Score 7; DB 16; Length 181;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 390 TDEIEK 396  
Db 106 TDEIEK 112

RESULT 69  
ID Q8V4S0 PRELIMINARY; PRT; 182 AA.  
AC Q8V4S0;  
DT 01-MAR-2002 (T-EMBLrel. 20, Created)  
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)  
DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)  
DE BBR.  
GN BBR.  
OS Monkeypox virus.  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Orthopoxvirus.  
OX NCBI\_TaxID=10244;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Zaire-96-I-16;  
RX MEDLINE=2159287; PubMed=11734207;  
RA Shchelkunov S.N., Totmenin A.V., Babkin I.V., Safronov P.F.,  
Ryazankina O.I., Petrov N.A., Gutorov V.V., Uvarova E.A.,  
Mikheev M.V., Sisler J.R., Eposito J.J., Jahrling P.B., Moss B.,  
Sandakhtchiev L.S.;  
RT "Human monkeypox and smallpox viruses: genomic comparison.";  
RL FEBS Lett. 509:66-70(2001).  
RN [2]

RP SEQUENCE FROM N.A.  
RC STRAIN=Zaire-96-I-16;  
RA Shchelkunov S.N., Totmenin A.V., Safronov P.F., Gutorov V.V.,  
Ryazankina O.I., Petrov N.A., Babkin I.V., Uvarova E.A.,  
Eposito J.J., Moss B., Sisler J.R., Jahrling P.B., Sandakhtchiev L.S.;  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF380138; AAL40627.1; -;  
SQ SEQUENCE 182 AA; 21488 MW; E248F33C227DC77C CRC64;

Query Match 1.7%; Score 7; DB 12; Length 182;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 SIITESC 144  
Db 62 SIITESC 68

RESULT 70  
ID Q9WGAL PRELIMINARY; PRT; 182 AA.  
AC Q9WGAL;  
DT 01-NOV-1999 (T-EMBLrel. 12, Created)  
DT 01-NOV-1999 (T-EMBLrel. 12, Last sequence update)  
DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)  
DE 21.3K protein (TB7R).  
GN B7R.  
OS Vaccinia virus (strain Tian Tan), and  
OS Vaccinia virus.  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Orthopoxvirus.  
OX NCBI\_TaxID=10253, 10245;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC SPECIES=Vaccinis virus; STRAIN=PRAHA;  
RA Stoller V., Ludvikova V., Maresova L., Nemeckova S., Vonka V.,  
RT "Effect of interferon gamma receptor gene deletion on Vaccinia virus  
RT virulence.";  
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=TIAN TAN;  
RA Jin Q., Hou Y.D., Cheng N.H., Yao E.M., Cheng S.X., Yang X.K.,  
Jing D.Y., Yu W.H., Yuan J.S., Ma X.J.;  
RT "Complete genomic sequence of vaccinia virus (Tian Tan strain).";  
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF120160; AAD22049.1; -;  
DR EMBL; AF095689; AAF34076.1; -;  
SQ SEQUENCE 182 AA; 21298 MW; 955DF62A1EEE6981 CRC64;

Query Match 1.7%; Score 7; DB 12; Length 182;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 SIITESC 144  
Db 62 SIITESC 68

RESULT 71  
ID O72743 PRELIMINARY; PRT; 182 AA.  
AC O72743;  
DT 01-AUG-1998 (T-EMBLrel. 07, Created)  
DT 01-AUG-1998 (T-EMBLrel. 07, Last sequence update)  
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)  
DE B6R protein.  
GN B6R.  
OS Cowpox virus (CPV).  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Orthopoxvirus.  
OX NCBI\_TaxID=10243;  
RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN=GRI-90;  
RX MEDLINE=97068532; PubMed=8963248;  
RA Saifonov P.F., Petrov N.A., Riazankina O.I., Totmenin A.V.,  
RA Shchelkunov S.N., Sandakhchiev L.S.;  
RT "Genes of a circle of hosts for the cowpox virus.";  
RL Dokl. Akad. Nauk 349:829-833(1996).  
[2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GRI-90;  
RA Shchelkunov S.N., Saifonov P.F., Totmenin A.V., Miheev M.V.,  
RA Ryzankina O.I., Petrov N.A., Gutorov V.V., Kotwal G.J.,  
RA Sandakhchiev L.S.;  
RT "Structure-function and organization of cowpox virus strain GRI-90  
complete genome.";  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
[3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GRI-90;  
RA Totmenin A.V.;  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; X94355; CAD90732.1; -;  
SQ SEQUENCE 182 AA; 21274 MW; 42BA561C312B757E CRC64;  
  
Query Match 1.7%; Score 7; DB 12; Length 182;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 138 SIITESC 144  
DB 62 SIITESC 68  
  
RESULT 72  
C022194  
ID C022194 PRELIMINARY; PRT; 185 AA.  
AC C022194;  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Putative proline-rich protein (Arabinogalactan protein AGP17).  
GN T20D16.24 OR AT2G23130.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eucotyledons; Brassicales; Brassicaceae; Arabidopsids.  
OX NCBI\_TaxID=3702;  
RN SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia;  
RA Rounsley S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C.,  
RA Sykes S.M., Kaul S., Mason T.M., Kerlavage A.R., Adams M.D.,  
RA Somerville C.R., Venter J.C.;  
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
[2]  
RP SEQUENCE FROM N.A.  
RA Gilson P., Gaspar Y.M., Oxley D., Youl J.J., Bacic A.;  
RT "NACP4 is an arabinogalactan protein whose expression is suppressed  
by wounding and fungal infection in Nicotiana glauca.";  
RL Protoplasma 0:0-0(2001).  
[3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia;  
RA Rounsley S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C.,  
RA Sykes S.M., Kaul S., Mason T.M., Kerlavage A.R., Adams M.D.,  
RA Somerville C.R., Venter J.C.;  
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
[4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia;  
RA Lin X.;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
[5]

RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia;  
RA Town C.D., Kaul S.;  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
[6]  
RP SEQUENCE FROM N.A.  
RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N.,  
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;  
RT "Full-length messenger RNA sequences greatly improve genome  
annotation.";  
RL Genome Biol. 0:0-0(2002).  
[7]  
RP SEQUENCE FROM N.A.  
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,  
RA Feldmann K.;  
RT "Full-length cDNA from Arabidopsis thaliana.";  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
[8]  
RP SEQUENCE FROM N.A.  
RA Yanada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,  
RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,  
RA Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,  
RA Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,  
RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,  
RA Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,  
RA Theologis A.;  
RT "Arabidopsis Full length cDNA Clones.";  
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
[9]  
RP SEQUENCE FROM N.A.  
RA Yanada K., Dale J.M., Hsuan V.W., Onodera C.S., Quach H.L., Chen H.,  
RA Toriumi M., Wong C., Wu H.C., Yu G., Yuan S., Carninci P., Chen H.,  
RA Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Kawai J.,  
RA Kim C.J., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,  
RA Seki M., Shinn P., Southwick A., Tripp M.G., Wu T., Shinozaki K.,  
RA Davis R.W., Ecker J.R., Theologis A.;  
RT "Arabidopsis Open Reading Frame (ORF) Clones.";  
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AC002391; AAB87117.1; -;  
DR EMBL; AF305939; AAG41563.1; -;  
DR EMBL; AC004401; AAM14931.1; -;  
DR EMBL; AY086875; AAM63921.1; -;  
DR EMBL; BT002926; AAC22741.1; -;  
DR EMBL; BT008601; AAP40426.1; -;  
DR PIR; T00519; T00519.  
SQ SEQUENCE 185 AA; 18481 MW; 64A10CD28BF8EBAC CRC64;  
  
Query Match 1.7%; Score 7; DB 10; Length 185;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 337 PASTPQI 343  
DB 76 PASTPQI 82  
  
RESULT 73  
P93674  
ID P93674 PRELIMINARY; PRT; 187 AA.  
AC P93674;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Putative 21kD protein precursor.  
OS Medicago sativa (Alfalfa).  
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eucotyledons; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.  
OX NCBI\_TaxID=3879;  
RN SEQUENCE FROM N.A.  
RC STRAIN=A2; Tissue=Nodele;  
RA Coronado C., Ratet P.;

Submitted (FEB-1997) to the EMBL/GenBank/DBSJ databases.  
RL EMBL: Y11553; CAA72315.1; -  
DR PIR: T09390; T09390.  
DR GO: GO:0016020; C:membrane; IEA.  
DR GO: GO:0004872; F:receptor activity; IEA.  
DR GO: GO:0005225; F:transporter activity; IEA.  
DR GO: GO:0006810; P:transport; IEA.  
DR InterPro: IPR007186; PME1.  
DR InterPro: IPR006501; PME inhib.  
DR Pfam: PF04043; PME1; 1.  
DR TIGRFAMs: TIGR01614; PME inhib; 1.  
DR PROSITE: PS00430; TONE\_DEPENDENT\_REC\_1; 1.  
KW Signal.  
FT SIGNAL.  
SQ SEQUENCE 187 AA; 20639 MW; BP60799E3166DFB5 CRC64;  
18  
POTENTIAL.  
Query Match 1.7%; Score 7; DB 10; Length 187;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 130 LVFLLLT 136  
DB 7 LVFLLLT 13  
RESULT 74  
Q9K802 PRELIMINARY; PRT; 190 AA.  
AC Q9K802;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Hypothetical protein BH2951.  
GN BH2951.  
OS Bacillus halodurans.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=86665;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C-125 / JCM 9153;  
RX MEDLINE=20512582; PubMed=11058132;  
RA Takami H., Nakasone K., Takaki Y., Masui N.,  
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,  
RA Horikoshi K.;  
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus  
RT halodurans and genomic sequence comparison with Bacillus subtilis."  
RL Nucleic Acids Res. 28:4317-4331(2000).  
DR EMBL: AP001517; BAB06670.1; -  
DR PIR: G84018; G84018.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 190 AA; 21832 MW; 71F988067DBB21DC CRC64;  
Query Match 1.7%; Score 7; DB 16; Length 190;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 165 PLVVANL 171  
DB 95 PLVVANL 101  
RESULT 75  
Q8SW02 PRELIMINARY; PRT; 201 AA.  
AC Q8SW02;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein ECU03\_1430.  
GN ECU03\_1430.  
OS Encephalitozoon cuniculi.  
OC Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.

NCBI\_TaxID=6035;  
[1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GB-M1;  
RA Genoscope;  
RL Submitted (APR-2001) to the EMBL/GenBank/DBSJ databases.  
[2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GB-M1;  
RX MEDLINE=21576510; PubMed=11719806;  
RA Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat P.,  
RA Frensch G., Barbe V., Peyretailade E., Brottier P., Wincker P.,  
RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,  
RA Weissbach J., Vivares C.P.;  
RT "Genome sequence and gene compaction of the eukaryote parasite  
RT Encephalitozoon cuniculi."  
RL Nature 414:450-453(2001).  
CC -1- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAS SUBFAMILY.  
DR EMBL: AL590443; CAD26286.1; -  
DR HSPF; P05713; 3RAB.  
DR GO: GO:0005225; F:GTP binding; IEA.  
DR GO: GO:0003928; F:RAB small monomeric GTPase activity; IEA.  
DR GO: GO:0015031; P:protein transport; IEA.  
DR GO: GO:0007264; P:small GTPase mediated signal transduction; IEA.  
DR InterPro: IPR003579; GTPase Rab.  
DR InterPro: IPR001806; Ras transfrmg.  
DR InterPro: IPR005225; Small\_GTP.  
DR Pfam: PF00071; Ras; 1.  
DR PRINTS: PR00449; RASTRNSFRMG.  
DR SMART: SM00175; RAB; 1.  
DR TIGRFAMs: TIGR00231; small GTP; 1.  
KW Hypothetical protein; GTP-Binding; Lipoprotein.  
SQ SEQUENCE 201 AA; 22832 MW; 3DE29F8A909619D0 CRC64;  
Query Match 1.7%; Score 7; DB 5; Length 201;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 390 TDEIEK 396  
DB 132 TDEIEK 138  
RESULT 76  
O77378 PRELIMINARY; PRT; 202 AA.  
AC O77378;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
GN PFC0795W; MAL386.18.  
OS Plasmodium falciparum (isolate 3D7).  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.  
OX NCBI\_TaxID=36329;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=3D7;  
RX MEDLINE=93376085; PubMed=10448855;  
RA Bowman S., Lawson D., Basham D., Brown D., Chillingworth T.,  
RA Churcher C.M., Craig A., Davies R.M., Devlin K., Feltwell T.,  
RA Gentles S., Gilliam R., Hamlin N., Harris D., Holroyd S., Hornsby T.,  
RA Horrocks P., Jagels K., Kysal B., Kyes S., McLean J., Moule S.,  
RA Mungall K., Murphy L., Oliver K., Quail M.A., Rajandream M.-A.,  
RA Rutter S., Skelton J., Squares R., Squares S., Sulston J.E.,  
RA Whitehead S., Woodward J.R., Newbold C., Barrell B.G.;  
RT "The complete nucleotide sequence of chromosome 3 of Plasmodium  
RT falciparum."  
RL Nature 400:532-538(1999).  
DR EMBL: Z98551; CAB1134.1; -  
DR PIR: T18495; T18495.  
KW Hypothetical protein.  
SQ SEQUENCE 202 AA; 24412 MW; 91D8293B96F71CE9 CRC64;

Query Match 1.7%; Score 7; DB 5; Length 202;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 LKKILSN 91  
DB 112 LKKILSN 118

RESULT 77  
Q9N9M4 PRELIMINARY; PRT; 216 AA.  
ID Q9N9M4  
AC Q9N9M4  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Probable possible programmed cell death protein, copy 1.  
GN L3665.02 OR P265.03.  
OS Leishmania major.  
OC Eukaryota; Eucelozoa; Kinetoplastida; Trypanosomatidae; Leishmania.  
OX NCBI\_TaxID=5684;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Friedlin;  
RA Aert R., Robben J., Weltjens I., Grymonprez B., Volckaert G.,  
RA Ivens A.C., Quail M., Rajandream M.A., Barrell B.G.;  
RL Submitted (Oct-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Friedlin;  
RX MEDLINE=98146435; PubMed=9477341;  
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,  
RA Smith D.F.;  
RT "A physical map of the Leishmania major Friedlin genome.";  
RL Genome Res. 8:135-145(1998).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Friedlin;  
RA Robben J., Grymonprez B., Weltjens I., Aert R., Volckaert G.,  
RA Ivens A.C., Quail M., Rajandream M.A., Barrell B.G.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL359775; CAB95247.1; -;  
DR EMBL; AL359716; CAC33967.1; -;  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR InterPro; IPR002048; EF-hand.  
DR Pfam; PF00036; ehand; 4.  
DR ProDom; PD000012; EF-hand; 1.  
DR SMART; SM00054; EPH; 2.  
DR PROSITE; PS00018; EF\_HAND; 2.  
SQ SEQUENCE 216 AA; 23808 MW; E384F6F1BF9DC278 CRC64;

Query Match 1.7%; Score 7; DB 5; Length 216;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LSGFVLG 16  
DB 146 LSGFVLG 152

RESULT 78  
Q9S436 PRELIMINARY; PRT; 220 AA.  
ID Q9S436  
AC Q9S436  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE M protein precursor (Fragment).  
GN EMM.  
OS Streptococcus pyogenes.  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
OC Streptococcus.

OX NCBI\_TaxID=1314;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SS1551;  
RA Beall B.;  
RT "New M protein gene sequence type st4264 from Malaysia isolate.";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF163684; AAD49332.1; -;  
DR GO; GO:0016020; C:membrane; IEA.  
DR InterPro; IPR003345; M\_repeat.  
DR InterPro; IPR002017; Spectrin.  
DR Pfam; PF02370; M; 1.  
DR Signal.  
KW NON TER 1 1  
FT SIGNAL <1 23 POTENTIAL.  
FT CHAIN 24 >220 M PROTEIN.  
FT NON TER 220 220  
SQ SEQUENCE 220 AA; 25597 MW; ED900EE15458D2E4 CRC64;

Query Match 1.7%; Score 7; DB 2; Length 220;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 KREIEKR 257  
DB 145 KREIEKR 151

RESULT 79  
Q8U0K7 PRELIMINARY; PRT; 221 AA.  
ID Q8U0K7  
AC Q8U0K7  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein PF1580.  
GN PFI580.  
OS Pyrococcus furiosus.  
OC Archaea; Euryarchaeota; Thermococci; Thermococcaceae;  
OC Pyrococcus.  
OX NCBI\_TaxID=2261;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Vcl / DSM 3638 / ATCC 43587 / JCM 8422;  
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;  
RT "The complete sequence of the Pyrococcus furiosus genome.";  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AE010258; AAL81704.1; -;  
DR GO; GO:0003676; F:nucleic acid binding; IEA.  
DR InterPro; IPR004087; KH\_dom.  
DR InterPro; IPR009019; KH\_prok.  
DR Pfam; PF00013; KH; 1.  
DR SMART; SM00322; KH; 2.  
DR PROSITE; PS50084; KH\_TYPE\_1; 2.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 221 AA; 25495 MW; 26C00FCBF8E47B9 CRC64;

Query Match 1.7%; Score 7; DB 17; Length 221;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 KREIEKR 257  
DB 58 KREIEKR 64

RESULT 80  
Q8ED42 PRELIMINARY; PRT; 227 AA.  
ID Q8ED42  
AC Q8ED42;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)



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DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Acyl-CoA thioesterase I, putative.
GN SO2928.
OS Shewanella oneidensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Shewanella.
OX NCBI_TaxID=70863;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NR-1;
RX MEDLINE=22297686; PubMed=12368813;
RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,
RA Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,
RA Madupu R., Peterson J.D., Umayam L.A., White C., Wolf A.M.,
RA Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,
RA Mueller J., Khouri H., Gill J., Uterback T.R., McDonald L.A.,
RA Feldblyum T.V., Smith H.O., Venter J.C., Nealon K.H., Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis.";
RL Nat. Biotechnol. 20:1118-1123 (2002).
RL EMBL; AF015731; JN55942.1; -.
DR TIGR; SO2928; -.
DR GO; GO:0003824; F: catalytic activity; IEA.
DR InterPro; IPR001087; Lipase_GDSL.
DR Pfam; PF00657; Lipase_GDSL; 1.
KW Complete proteome.
SQ SEQUENCE 227 AA; 25117 MW; 40466A0F8BFB9CA4 CRC64;

Query Match 1.7%; Score 7; DB 16; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 GMSEQLG 178
DB 64 GMSEQLG 70
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RESULT 81
ID O01329 PRELIMINARY; PRT; 228 AA.
AC O01329;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE F46A8.3 protein.
DE F46A8.3
GN Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Harris B.R.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018 (1998).
DR EMBL; Z81539; CAB04389.1; -.
DR PIR; T22259; T22259.
DR WormPep; F46A8.3; CE10562.
DR InterPro; IPR008985; ConA-like lec_gl.
DR InterPro; IPR001079; Galactin.
DR Pfam; PF00337; Gal-bind lectin; 1.
DR SMART; SM00276; GLECT; 1.
SQ SEQUENCE 228 AA; 26022 MW; B82D33036F1EBB0F CRC64;

Query Match 1.7%; Score 7; DB 5; Length 228;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 VLGLAF 20
DB 207 VLGLAF 213
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RESULT 83
ID Q9K6G9 PRELIMINARY; PRT; 237 AA.
AC Q9K6G9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE ATP synthase A chain (protein 6).
DE ATP OR BH3760.
GN Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331 (2000).
CC -!- FUNCTION: KEY COMPONENT OF THE PROTON CHANNEL; IT MAY PLAY A
CC DIRECT ROLE IN THE TRANSLOCATION OF PROTONS ACROSS THE MEMBRANE
CC (BY SIMILARITY).
CC -!- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS. CF(1) - THE CATALYTIC
CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE

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Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 LVFLLLT 136
DB 3 LVFLLLT 9
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RESULT 82
ID Q8Y2U4 PRELIMINARY; PRT; 236 AA.
AC Q8Y2U4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Putative peremease transmembrane protein.
GN RSC0338 OR RS00670.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GMI1000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Bottier P., Camus J.C., Catolico L.,
RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gagnier P., Moisan A., Robert C., Saurin W., Schiex T.,
RA Siguer P., Thebault P., Whalen M., Wincker F., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502 (2002).
DR EMBL; AL646058; CAD13766.1; -.
KW Complete proteome.
SQ SEQUENCE 236 AA; 24140 MW; 54417628C19BE432 CRC64;

Query Match 1.7%; Score 7; DB 16; Length 236;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 VLGLAF 20
DB 207 VLGLAF 213
|||||

RESULT 83
ID Q9K6G9 PRELIMINARY; PRT; 237 AA.
AC Q9K6G9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE ATP synthase A chain (protein 6).
GN ATP OR BH3760.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331 (2000).
CC -!- FUNCTION: KEY COMPONENT OF THE PROTON CHANNEL; IT MAY PLAY A
CC DIRECT ROLE IN THE TRANSLOCATION OF PROTONS ACROSS THE MEMBRANE
CC (BY SIMILARITY).
CC -!- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS. CF(1) - THE CATALYTIC
CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE

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CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)  
 CC HAS THREE MAIN SUBUNITS: A, B AND C (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE ATPASE A CHAIN FAMILY.  
 CC EMBL: A2001519; BAB07479.1; -.  
 CC FIR; H84119; H84119.  
 CC DR HSSP; P00855; ICI17.  
 CC DR GO; GO:0016021; C: integral to membrane; IEA.  
 CC DR GO; GO:0015078; F: hydrolase ion transporter activity; IEA.  
 CC DR GO; GO:0016787; F: hydrolase activity; IEA.  
 CC DR GO; GO:0015992; P: proton transport; IEA.  
 CC DR InterPro; IPR000568; ATPsynth\_Asub.  
 CC DR Pfam; PF00119; ATP\_synth\_A; 1.  
 CC DR PRINTS; PR0123; ATPASEA.  
 CC DR TIGRFAMs; TIGR01131; ATP\_synth\_6\_or\_A; 1.  
 CC DR PROSITE; PS00449; ATPASE\_A; 1.  
 CC KW CF(0); Hydorgen ion transport; Hydrolase; Transmembrane;  
 KW Complete proteome.  
 CC SEQUENCE 237 AA; 26974 MW; 6184C9BB0B401998 CRC64;

Query Match 1.7%; Score 7; DB 16; Length 237;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 397 MKGFGEY 403  
 DB 135 MKGFGEY 141

## RESULT 84

Q9NJQ3 ID Q9NJQ3 PRELIMINARY; PRT; 239 AA.  
 AC Q9NJQ3  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Triptophan hydroxylase (Fragment).  
 OS Lymnaea stagnalis (Great pond snail).  
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;  
 CC Lymnaeidae; Lymnaeidae; Lymnaea.  
 CC NCBI\_TaxID=6523;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21359676; PubMed=11466431;  
 RA Koert C.E., Spencer G.E., van Minnen J., Li K.W., Geraerts W.P.,  
 RA Syed N.I., Smit A.B., van Kesteren R.E.;  
 RA "Functional implications of neurotransmitter expression during axonal  
 RT regeneration: serotonin, but not peptides, auto-regulate axon growth  
 RT of an identified central neuron.";  
 RL J. Neurosci. 21:5597-5606(2001).  
 DR EMBL; AF129815; AAF36488.1; -.  
 DR HSSP; P04176; 1PHZ.  
 DR GO; GO:0005506; F: iron ion binding; IEA.  
 DR GO; GO:0004497; F: monooxygenase activity; IEA.  
 DR GO; GO:0009072; P: aromatic amino acid family metabolism; IEA.  
 DR InterPro; IPR001273; Aaa hydroxylase.  
 DR Pfam; PF00351; biotpterin\_H; 1.  
 DR PRINTS; PR00372; FWHYDRXLASE.  
 DR ProDom; PD002559; Aaa hydroxylase; 1.  
 DR PROSITE; PS00367; BIOTPTERIN\_HYDROXYL; 1.  
 FT NON\_TER 1  
 FT NON\_TER 239  
 SQ SEQUENCE 239 AA; 28001 MW; D721BD16C7D7B194 CRC64;

Query Match 1.7%; Score 7; DB 5; Length 239;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 VNRKKE 253  
 DB 29 VNRKKE 35

## RESULT 85

Q816W1 ID Q816W1 PRELIMINARY; PRT; 242 AA.  
 AC Q816W1  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Ribosomal small subunit pseudouridine synthase A (EC 4.2.1.70).  
 GN BC4704.  
 OS Bacillus cereus (strain ATCC 14579 / DSM 31).  
 CC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 CC NCBI\_TaxID=226900;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22608415; PubMed=12721630;  
 RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,  
 RA Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,  
 RA Chu L., Mazur M., Goltzman E., Larsen N., D'Souza M., Walunas T.,  
 RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,  
 RA Overbeek R., Kyrgides N.;  
 RT "Genome sequence of *Bacillus cereus* and comparative analysis with  
 RT *Bacillus anthracis*.";  
 RL Nature 423:87-91(2003).  
 DR EMBL; AE017013; AAP11609.1; -.  
 DR GO; GO:0016829; F: lyase activity; IEA.  
 DR GO; GO:0004730; F: pseudouridylate synthase activity; IEA.  
 DR GO; GO:0003723; F: RNA binding; IEA.  
 DR InterPro; IPR006145; Pseudou synth.  
 DR InterPro; IPR000748; Psi\_synth\_RSU.  
 DR InterPro; IPR002942; S4.  
 DR Pfam; PF00849; Pseudou synth\_2; 1.  
 DR Pfam; PF01479; S4; 1.  
 DR SMART; SM00363; S4; 1.  
 DR TIGRFAMs; TIGR00093; TIGR00093; 1.  
 DR PROSITE; PS01149; PSI\_RSU; 1.  
 DR PROSITE; PS00889; S4; 1.  
 KW Lyase; Complete proteome.  
 SQ SEQUENCE 242 AA; 27503 MW; 6B6B4557FE60F9CB CRC64;

Query Match 1.7%; Score 7; DB 16; Length 242;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 DTGFFLL 34  
 DB 105 DTGFFLL 111

## RESULT 86

Q8K1L4 ID Q8K1L4 PRELIMINARY; PRT; 244 AA.  
 AC Q8K1L4  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Similar to C-type (Calcium dependent, carbohydrate recognition domain)  
 DE lectin, superfamily member 12.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC027742; AAH27742.1; -.  
 DR GO; GO:0005529; F: sugar binding; IEA.  
 DR InterPro; IPR002353; AntifreezeII.  
 DR InterPro; IPR001304; Lectin\_C.  
 DR Pfam; PF00059; lectin\_c; 1.  
 DR PRINTS; PR00356; ANTIFREEZEII.  
 DR SMART; SM00034; CLECT; 1.  
 DR PROSITE; PS50041; C\_TYPE\_LECTIN\_2; 1.

SQ SEQUENCE 244 AA; 27542 MW; F50158025FA80C2A CRC64;  
Query Match 1.7%; Score 7; DB 11; Length 244;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 14 VLGAALAF 20  
Db 63 VLGAALAF 69  
RESULT 87  
Q9J150 PRELIMINARY; PRT; 244 AA.  
AC Q9J150;  
DT 01-OCT-2000 (TREMELrel. 15, Created)  
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)  
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
DE Dendritic cell-associated C-type lectin-1.  
GN CLECSF12 OR DECTIN-1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALE/c;  
RX MEDLINE=20347934; PubMed=10779524;  
RA Arizumi K., Shen G.-L., Shikano S., Xu S., Ritter R. III,  
RA Kumamoto T., Edelbaum D., Morita A., Bergstresser P.R., Takashima A.;  
RT "Identification of a novel, dendritic cell-associated molecule,  
RT lectin-1, by subtractive cDNA cloning."  
RL J. Biol. Chem. 275:20157-20167(2000).  
DR EMBL; AF262985; AAF72710.1; -.  
DR MGD; MGI:1861431; Clecsf12.  
DR GO; GO:0005529; F:sugar binding; IEA.  
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.  
DR InterPro; IPR001304; Lectin\_C.  
DR Pfam; PF00059; lectin\_c; 1.  
DR SMART; SM00034; CLECT; 1.  
DR PROSITE; PS00041; C\_TYPE\_LLECTIN\_2; 1.  
KW Lectin.  
SQ SEQUENCE 244 AA; 27621 MW; 55A71C04E68CA002 CRC64;  
Query Match 1.7%; Score 7; DB 11; Length 244;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 14 VLGAALAF 20  
Db 63 VLGAALAF 69  
RESULT 88  
Q95LW2 PRELIMINARY; PRT; 245 AA.  
AC Q95LW2;  
DT 01-DEC-2001 (TREMELrel. 19, Created)  
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)  
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecinae; Macaca.  
OX NCBI\_TaxID=9541;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Testis;  
RA Hashimoto K., Osada N., Hida M., Kusuda J., Tanuma R., Hirai M.,  
RA Terao K., Sugano S.;  
RT "Isolation of novel full-length cDNA clones from macaque testis cDNA  
libraries."

RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB071079; BAB64472.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 245 AA; 28822 MW; 2B0B5FC4E969CF03 CRC64;  
Query Match 1.7%; Score 7; DB 6; Length 245;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 31 GFLGGEV 37  
Db 31 GFLGGEV 37  
RESULT 89  
Q9SNW9 PRELIMINARY; PRT; 245 AA.  
AC Q9SNW9;  
DT 01-MAY-2000 (TREMELrel. 13, Created)  
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)  
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
DE Putative transcription factor (transcription factor-like).  
GN MYB99.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia;  
RA Stracke R., Weisshaar B.;  
RT "R2R3-MYB transcription factor gene nomenclature in Arabidopsis  
RT thaliana".  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=COLUMBIA;  
RX MEDLINE=20181125; PubMed=10718197;  
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,  
RA Tabata S.;  
RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence  
RT features of the regions of 3,076,755 bp covered by sixty PI and TAC  
RT clones".  
RL DNA Res. 7:31-63(2000).  
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
CC -1- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.  
DR EMBL; AF199026; AAF06022.1; -.  
DR EMBL; AB019235; BAA97196.1; -.  
DR HSRP; P06876; IMBK.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR InterPro; IPR001005; Myb\_DNA\_binding.  
DR Pfam; PF00249; myb\_DNA-binding; 2.  
DR SMART; SM00717; SANT; 2.  
DR PROSITE; PS00037; MYB\_1; 1.  
DR PROSITE; PS00334; MYB\_2; 1.  
DR PROSITE; PS00090; MYB\_3; 2.  
KW DNA-binding; Nuclear protein.  
SQ SEQUENCE 245 AA; 27356 MW; D41F6850ADCE7A49 CRC64;  
Query Match 1.7%; Score 7; DB 10; Length 245;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 TSAVLGS 12  
Db 169 TSAVLGS 175  
RESULT 90  
Q8IB21 PRELIMINARY; PRT; 247 AA.  
ID Q8IB21

AC Q8IB21,  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical protein.  
 GN MAL8P1.66.  
 OS Plasmodium falciparum (isolate 3D7).  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=36329;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Seeger K., Murphy L., Harris D., Berriman M., Pain A., Hall N.,  
 RA Quail M., Barrell B.;  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBSJ databases.  
 DR EMBL; AL844507; CAD51198.1; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 247 AA; 28410 MW; ACC5E50E7E220CDA CRC64;  
 Query Match 1.7%; Score 7; DB 5; Length 247;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 266 REKNIQK 272  
 DB 231 REKNIQK 237  
 RESULT 91  
 Q82VV9 PRELIMINARY; PRT; 247 AA.  
 AC Q82VV9;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Survival protein SurE.  
 GN SURE OR NE0950.  
 OS Nitrosomonas europaea.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;  
 OC Nitrosomonadaceae; Nitrosomonas.  
 OX NCBI\_TaxID=915;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 19718 / IFO 14298;  
 RX MEDLINE=22586410; PubMed=12700255;  
 RA Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.,  
 RA Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,  
 RA Arciero D.M., Holmes N.G., Whittaker M.M., Arp D.J.;  
 RT "Complete genome sequence of the ammonia-oxidizing bacterium and  
 RT obligate chemolithoautotroph Nitrosomonas europaea."  
 RL J. Bacteriol. 185:2759-2773 (2003).  
 DR EMBL; BX321859; CAD84861.1; -;  
 DR InterPro; IPR002828; SurE.  
 DR Pfam; PF01975; SurE; 1.  
 DR ProDom; PD005378; SurE; 1.  
 DR TIGRFAMs; TIGR00087; surE; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 247 AA; 26851 MW; 173C0E7104B384D1 CRC64;  
 Query Match 1.7%; Score 7; DB 16; Length 247;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 29 TEGFLIG 35  
 DB 110 TEGFLIG 116  
 RESULT 92  
 Q97J11 PRELIMINARY; PRT; 254 AA.  
 ID Q97J11  
 AC Q97J11;  
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)  
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DS Proline/glycine betaine ABC transport system, ATPase  
 DE component.  
 GN CAC1475.  
 OS Clostridium acetobutylicum.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 OX NCBI\_TaxID=1488;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;  
 RX MEDLINE=21359325; PubMed=11466286;  
 RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,  
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,  
 RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,  
 RA Bennett G.N., Koonin E.V., Smith D.R.;  
 RT "Genome sequence and comparative analysis of the solvent-producing  
 RT bacterium Clostridium acetobutylicum."  
 RL J. Bacteriol. 183:4823-4838 (2001).  
 DR EMBL; AE007558; AAK79443.1; -;  
 DR PIR; H97081; H97081.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. .; IEA.  
 DR GO; GO:0000166; F:nucleotide binding; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR003593; AAA\_ATPase.  
 DR InterPro; IPR003439; ABC\_transporter.  
 DR Pfam; PF00005; ABC\_tran; 1.  
 DR ProDom; PD00006; ABC\_transporter; 1.  
 DR SMART; SM00382; AAA; 1.  
 DR PROSITE; PS00211; ABC\_TRANSPORTER\_1; 1.  
 DR PROSITE; PS00893; ABC\_TRANSPORTER\_2; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 254 AA; 28845 MW; 5172AE8B4EEAD3BA CRC64;  
 Query Match 1.7%; Score 7; DB 16; Length 254;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 251 KREIEKR 257  
 DB 111 KREIEKR 117  
 RESULT 93  
 Q97Q44 PRELIMINARY; PRT; 257 AA.  
 ID Q97Q44  
 AC Q97Q44;  
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)  
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Spermidine/putrescine ABC transporter, permealase protein.  
 GN SPI387.  
 OS Streptococcus pneumoniae.  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 OX NCBI\_TaxID=1313;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC BAA-334 / TIGR4;  
 RX MEDLINE=21357209; PubMed=11463916;  
 RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,  
 RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,  
 RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,  
 RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,  
 RA Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,  
 RA McDonald L.E., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,  
 RA Holt I.E., Loftus B.J., Yang P., Smith H.O., Venter J.C.,  
 RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;  
 RT "Complete genome sequence of a virulent isolate of Streptococcus  
 RT pneumoniae."  
 RL Science 293:498-506 (2001).

DR EMBL; AE007436; AAK75485.1; -.  
 DR PIR; D95161; D95161.  
 DR TIGR; SPI387; -.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005215; F:transporter activity; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR000515; BPD\_transp.  
 DR Pfam; PF00528; BPD\_transp; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 257 AA; 28978 MW; 4619D7D6328E8C4C CRC64;  
 Query Match 1.7%; Score 7; DB 16; Length 257;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 135 LTFSIIT 141  
 Db 179 LTFSIIT 185  
 ID Q9ALL2 PRELIMINARY; PRT; 258 AA.  
 AC Q9ALL2;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE CS12 fibria upstream putative regulatory protein.  
 GN YAHF.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=350CI;  
 RA Steinland H., Gaastra W., Valvatne H., Sommerfelt H.;  
 RT "The organization of the enterotoxigenic Escherichia coli CS12 gene cluster is identical to that of the 987P gene cluster";  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE ARAC/XYLS FAMILY OF TRANSCRIPTIONAL REGULATORS.  
 CC EMBL; AY009096; AAK0965.1; -.  
 DR GO; GO:0005622; C:intracellular; IEA.  
 DR GO; GO:0003700; F:transcription factor activity; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR GO; GO:0006350; P:transcription; IEA.  
 DR InterPro; IPR000005; HTHARAC.  
 DR Pfam; PF00165; HTH\_ARAC; 2.  
 DR PRINTS; PR00032; HTHARAC.  
 DR SMART; SM00342; HTH\_ARAC; 1.  
 DR PROSITE; PS00041; HTH\_ARAC\_FAMILY\_1; 1.  
 DR PROSITE; PS01124; HTH\_ARAC\_FAMILY\_2; 1.  
 KW DNA-binding; Transcription; Transcription regulation.  
 SQ SEQUENCE 258 AA; 28616 MW; 35776C84B93CPE8B CRC64;  
 Query Match 1.7%; Score 7; DB 2; Length 258;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
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 QY 84 ALKKILS 90  
 Db 73 ALKKILS 79  
 ID Q7WZ08 PRELIMINARY; PRT; 264 AA.  
 AC Q7WZ08;  
 DT 01-OCT-2003 (TREMBLrel. 25, Created)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE S-adenosylmethionine decarboxylase.

GN SPED.  
 OS Lysobacter enzymogenes.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;  
 OC Xanthomonadaceae; Lysobacter.  
 OX NCBI\_TaxID=69;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C3;  
 RA Kobayashi D.Y., Reedy R.M., Palumbo J.D., Yuen G.Y.;  
 RT "Transposon insertion within a catabolite activator protein-like protein (cip) gene homolog results in loss of lytic enzyme, antifungal RT and biological control activities expressed by Lysobacter enzymogenes strain C3";  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY316743; AAP83140.1; -. 5D28C7061A412C53 CRC64;  
 SQ SEQUENCE 264 AA; 30594 MW;  
 Query Match 1.7%; Score 7; DB 2; Length 264;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 249 RLKREIE 255  
 Db 248 RLKREIE 254  
 ID Q97QX9 PRELIMINARY; PRT; 266 AA.  
 AC Q97QX9;  
 DT 01-OCT-2001 (TREMBLrel. 18, Created)  
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE AEC-2 transporter, permease protein, putative.  
 GN SPI063.  
 OS Streptococcus pneumoniae.  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 OX NCBI\_TaxID=1313;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC BAA-334 / TIGR4;  
 RX MEDLINE=21357209; PubMed=11463916;  
 RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D., Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C., McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;  
 RT "Complete genome sequence of a virulent isolate of Streptococcus pneumoniae";  
 RL Science 293:498-506(2001).  
 DR EMBL; AE007408; AAK75177.1; -.  
 DR PIR; H95122; H95122.  
 DR TIGR; SPI063; -.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. .; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR000412; ABC\_transpt2.  
 DR PRINTS; PR00164; ABC2TRANSPORT.  
 KW Complete proteome.  
 SQ SEQUENCE 266 AA; 30501 MW; F3AA416DC89F4883 CRC64;  
 Query Match 1.7%; Score 7; DB 16; Length 266;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
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Q8ZJC0
ID Q8ZJC0 PRELIMINARY; PRT; 266 AA.
AC Q8ZJC0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8).
GN FKPA OR YP00135.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360;
RA Parhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebathia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Fellwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
DR EMBL; AJ414141; CAC89056.1; -.
DR PIR; AF0024; AF0024.
DR GO; GO:0042027; F:cytrophilin-type peptidyl-prolyl cis-trans . . . ; IEA.
DR GO; GO:0004600; F:cytrophilin; IEA.
DR GO; GO:0030053; F:FK506-sensitive peptidyl-prolyl cis-trans i . . . ; IEA.
DR GO; GO:0006853; F:isomerase activity; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR InterPro; IPR000774; FKBP_Nterm.
DR Pfam; PF00254; FKBP_1.
DR Pfam; PF01346; FKBP_N; 1.
DR ProDom; PD001516; FKBP_Nterm; 1.
DR PROSITE; PS00454; FKBP_PPIASE_2; 1.
DR PROSITE; PS00559; FKBP_PPIASE_3; 1.
KW Isomerase; Complete proteome.
SQ SEQUENCE 266 AA; 28573 MW; 1BA343594FFEB4F CRC64;

Query Match 1.7%; Score 7; DB 15; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 390 TDEIEK 396
Db 91 TDEIEK 97
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RESULT 98
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ID Q9LH18 PRELIMINARY; PRT; 269 AA.
AC Q9LH18;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN F28J15.4.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.

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[2]
SEQUENCE FROM N.A.
STRAIN=COLUMBIA;
PubMed=10907853;
Nakamura Y.;
"Structural analysis of Arabidopsis thaliana chromosome 3. II.
Sequence features of the regions of 4,251,695 bp covered by ninety P1,
TAC and BAC clones.";
DNA Res. 7:217-221(2000).
[3]
SEQUENCE FROM N.A.
STRAIN=cv Columbia;
MEDLINE=21016720; PubMed=11130713;
RA Salanoubat M., Lemcke K., Rieger M., Ansong W., Unseld M.,
RA Fartmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
RA Delserny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA De Simone V., Choien N., Attiguenave F., Robert C., Brottier P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbech E., Drzonek H., Erle H., Jordan N., Bangert S.,
RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppi S., Simonati B.,
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordsiek G.,
RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RA Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA Monfort A., Argirou A., Flores M., Liguori R., Vitale D.,
RA Mannhaupt G., Haase D., Schoof H., Rued S., Zaccaria P., Mewes H.-W.,
RA Mayer K.P.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Pai G., Millscher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Preuss D., Lin X., Niernan W.C., Salzberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Ideawaka K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
thaliana.";
RL Nature 408:820-822(2000).
DR EMBL; AP002047; BAB03127.1; -.
DR EMBL; AP002063; BAB03127.1; JOINED.
DR EMBL; AC069472; AAG51075.1; -.
KW Hypothetical protein.
SQ SEQUENCE 269 AA; 32632 MW; D158FAD5E8659CA4 CRC64;

Query Match 1.7%; Score 7; DB 10; Length 269;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 249 RLKREIE 255
Db 105 RLKREIE 111
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RESULT 99
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ID Q8D8F1 PRELIMINARY; PRT; 270 AA.
AC Q8D8F1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Conserved hypothetical protein.
GN V13029.
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=672;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMCP6;

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Search completed: April 16, 2004, 10:20:34  
Job time : 68 secs

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RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RA Choy H.B.;
RT "Complete genome sequence of Vibrio vulnificus CMCP6";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AE016807; AAO11353.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 270 AA; 31639 MW; 56D7E1C98598156B CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 16; Length 270;
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AC Q8PE22;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ABC transporter ATP-binding protein.
GN YIMA OR XCC0161.
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=340;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33913 / NCPPB 528;
RX MEDLINE=22022145; PubMed=12024117;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Canavari F., Cardozo J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White P.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
DR EMBL; AE012112; AAM39480.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003439; ABC transporter.
DR Pfam; PF00005; ABC tran; 1.
DR PRODOM; PD000006; ABC transporter; 1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 278 AA; 30220 MW; 69B229E9E8921ADE CRC64;

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GenCore version 5.1.6  
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Gapop 60.0 , Gapext 60.0

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- 2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*
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- 6: /cgn2\_6/ptodata/2/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	151	36.9	151	4	US-09-621-976-3917
2	7	1.7	105	4	US-09-543-681A-6080
3	7	1.7	111	4	US-09-328-352-5992
4	7	1.7	117	4	US-09-621-976-4623
5	7	1.7	126	4	US-09-453-195A-4
6	7	1.7	137	3	US-09-446-504-34
7	7	1.7	137	4	US-09-712-266-34
8	7	1.7	182	4	US-09-540-236-2904
9	7	1.7	244	3	US-08-772-440-2
10	7	1.7	257	1	US-07-956-700B-105
11	7	1.7	257	1	US-08-476-537-105
12	7	1.7	257	1	US-08-485-607-105
13	7	1.7	257	2	US-08-475-879-105
14	7	1.7	257	4	US-09-433-043B-105
15	7	1.7	281	1	US-07-941-523-23
16	7	1.7	286	4	US-09-540-236-2036
17	7	1.7	296	1	US-08-320-161-11
18	7	1.7	296	1	US-08-137-175A-3
19	7	1.7	296	3	US-08-479-017-3
20	7	1.7	296	3	US-08-455-829-11
21	7	1.7	296	3	US-08-335-836C-22
22	7	1.7	296	4	US-08-455-973-11
23	7	1.7	319	4	US-09-910-174B-12
24	7	1.7	319	4	US-09-620-461-12
25	7	1.7	321	3	US-08-748-506-13
26	7	1.7	342	2	US-08-724-294A-6
27	7	1.7	357	4	US-09-910-174B-14

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29	7	1.7	380	3	US-08-235-836C-118	Sequence 118, App
30	7	1.7	393	3	US-08-235-836C-114	Sequence 114, App
31	7	1.7	417	4	US-09-252-991A-20165	Sequence 20165, A
32	7	1.7	441	3	US-08-235-836C-120	Sequence 120, App
33	7	1.7	448	3	US-08-878-989-2	Sequence 2, Appli
34	7	1.7	448	3	US-09-272-796-2	Sequence 2, Appli
35	7	1.7	454	3	US-08-235-836C-116	Sequence 116, App
36	7	1.7	495	4	US-09-328-352-4637	Sequence 4637, App
37	7	1.7	502	4	US-09-134-001C-3598	Sequence 3598, App
38	7	1.7	508	3	US-09-344-700-4	Sequence 4, Appli
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40	7	1.7	522	4	US-09-252-991A-16994	Sequence 16994, A
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54	7	1.7	1568	4	US-09-459-065-2	Sequence 2, Appli
55	6	1.5	9	1	US-08-462-128-28	Sequence 28, Appl
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57	6	1.5	9	3	US-09-171-705-77	Sequence 77, Appl
58	6	1.5	10	1	US-08-199-508-57	Sequence 57, Appl
59	6	1.5	11	3	US-08-932-272-46	Sequence 46, Appl
60	6	1.5	11	4	US-09-036-039-46	Sequence 46, Appl
61	6	1.5	16	3	US-09-171-705-55	Sequence 55, Appl
62	6	1.5	16	3	US-09-171-705-56	Sequence 56, Appl
63	6	1.5	18	4	US-09-205-258-1052	Sequence 1052, Ap
64	6	1.5	18	4	US-09-205-258-1053	Sequence 1053, Ap
65	6	1.5	18	5	PCT-US93-07653-1	Sequence 1, Appli
66	6	1.5	19	3	US-08-795-430-51	Sequence 51, Appl
67	6	1.5	19	4	US-09-355-700-51	Sequence 51, Appl
68	6	1.5	23	6	5368712-4	Patent No. 5368712
69	6	1.5	23	6	5516890-4	Patent No. 5516890
70	6	1.5	25	3	US-08-772-440-6	Sequence 6, Appli
71	6	1.5	26	3	US-08-912-272-44	Sequence 44, Appl
72	6	1.5	26	4	US-09-026-039-44	Sequence 44, Appl
73	6	1.5	26	4	US-09-156-856-14	Sequence 14, Appl
74	6	1.5	36	4	US-09-205-258-555	Sequence 555, App
75	6	1.5	39	4	US-09-315-304B-1459	Sequence 1459, Ap
76	6	1.5	39	4	US-09-515-965A-1459	Sequence 1459, Ap
77	6	1.5	39	4	US-09-350-641C-1459	Sequence 1459, Ap
78	6	1.5	46	3	US-09-124-671-5	Sequence 5, Appli
79	6	1.5	46	4	US-08-679-433A-170	Sequence 170, App
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82	6	1.5	60	3	US-09-167-681-43	Sequence 43, Appl
83	6	1.5	66	4	US-08-936-165A-291	Sequence 291, App
84	6	1.5	66	4	US-09-134-000C-4727	Sequence 4727, Ap
85	6	1.5	66	4	US-09-716-129-52	Sequence 52, Appl
86	6	1.5	67	4	US-09-149-476-430	Sequence 430, App
87	6	1.5	69	4	US-09-308-003-15	Sequence 15, Appl
88	6	1.5	73	1	US-08-280-443-25	Sequence 25, Appl
89	6	1.5	73	1	US-08-457-459-25	Sequence 25, Appl
90	6	1.5	73	1	US-08-555-678-25	Sequence 25, Appl
91	6	1.5	73	5	PCT-US95-02375-25	Sequence 6090, Ap
92	6	1.5	74	4	US-09-621-976-6090	Sequence 13015, A
93	6	1.5	75	4	US-09-489-039A-13015	Sequence 13015, A
94	6	1.5	80	1	US-07-881-075-16	Sequence 16, Appl
95	6	1.5	80	1	US-08-120-827-16	Sequence 16, Appl
96	6	1.5	80	1	US-08-478-675-16	Sequence 16, Appl
97	6	1.5	88	4	US-09-621-976-3983	Sequence 3983, Ap
98	6	1.5	91	3	US-08-851-843A-220	Sequence 220, App
99	6	1.5	91	3	US-08-974-549A-339	Sequence 339, App
100	6	1.5	91	3	US-08-854-050-220	Sequence 220, App



101	6	1.5	91	4	US-09-430-323-220	Sequence 220, App	174	6	1.5	192	2	US-09-008-180-4	Sequence 4, Appli
102	6	1.5	91	4	US-09-402-181B-339	Sequence 339, App	175	6	1.5	192	4	US-09-303-120B-8	Sequence 8, Appli
103	6	1.5	91	4	US-09-721-456-339	Sequence 339, App	176	6	1.5	192	4	US-09-820-576-8	Sequence 8, Appli
104	6	1.5	94	4	US-09-621-976-4628	Sequence 4628, App	177	6	1.5	194	4	US-09-489-039A-7974	Sequence 7974, Ap
105	6	1.5	96	4	US-09-134-000C-4033	Sequence 4033, Ap	178	6	1.5	195	4	US-09-858-664A-11	Sequence 11, Appl
106	6	1.5	103	2	US-08-539-878B-41	Sequence 41, Appl	179	6	1.5	195	4	US-10-374-978-12	Sequence 12, Appl
107	6	1.5	103	4	US-08-621-976-5415	Sequence 5415, Ap	180	6	1.5	195	4	US-08-446-925-7	Sequence 7, Appli
108	6	1.5	104	4	US-08-621-976-6748	Sequence 6748, Ap	181	6	1.5	204	2	US-09-146-331-7	Sequence 7, Appli
109	6	1.5	105	4	US-09-540-336-2606	Sequence 2606, Ap	182	6	1.5	204	2	US-08-896-885-7	Sequence 7, Appli
110	6	1.5	108	4	US-09-252-991A-21579	Sequence 21579, A	183	6	1.5	204	4	US-09-375-256-7	Sequence 7, Appli
111	6	1.5	108	4	US-08-543-881A-7196	Sequence 7196, Ap	184	6	1.5	204	4	US-09-376-156-7	Sequence 7, Appli
112	6	1.5	109	3	US-08-124-671-29	Sequence 29, Appl	185	6	1.5	204	4	US-09-252-991A-31809	Sequence 31809, A
113	6	1.5	110	4	US-09-308-453-3	Sequence 3, Appli	186	6	1.5	206	1	US-08-197-793-2	Sequence 2, Appli
114	6	1.5	113	4	US-09-328-352-5341	Sequence 5341, Ap	187	6	1.5	206	2	US-08-636-176-2	Sequence 2, Appli
115	6	1.5	117	5	PCT-US96-08730-11	Sequence 11, Appli	188	6	1.5	206	5	PCT-US95-01618-2	Sequence 2, Appli
116	6	1.5	118	1	US-07-988-273-3	Sequence 3, Appli	189	6	1.5	209	4	US-09-352-991A-29897	Sequence 29897, A
117	6	1.5	118	4	US-09-107-532A-6327	Sequence 6327, Ap	190	6	1.5	209	4	US-09-198-452A-138	Sequence 138, App
118	6	1.5	118	5	PCT-US93-12019-3	Sequence 3, Appli	191	6	1.5	209	4	US-09-489-039A-13642	Sequence 13642, A
119	6	1.5	119	3	US-08-513-974B-50	Sequence 50, Appl	192	6	1.5	210	1	US-08-848-932-2	Sequence 2, Appli
120	6	1.5	119	3	US-08-513-974B-354	Sequence 354, App	193	6	1.5	210	2	US-09-008-180-2	Sequence 2, Appli
121	6	1.5	119	3	US-08-513-974B-355	Sequence 355, App	194	6	1.5	211	4	US-08-540-236-2720	Sequence 2720, Ap
122	6	1.5	119	4	US-08-461-436B-50	Sequence 50, Appl	195	6	1.5	213	4	US-09-543-881A-5886	Sequence 5886, Ap
123	6	1.5	119	4	US-09-328-352-5915	Sequence 5915, Ap	196	6	1.5	214	4	US-09-328-352-6043	Sequence 6043, Ap
124	6	1.5	126	4	US-09-252-991A-24324	Sequence 24324, A	197	6	1.5	217	4	US-08-630-915A-225	Sequence 225, App
125	6	1.5	132	2	US-08-649-991-65	Sequence 65, Appl	198	6	1.5	217	4	US-09-252-991A-30641	Sequence 30641, A
126	6	1.5	132	4	US-09-489-039A-10292	Sequence 10292, A	199	6	1.5	219	4	US-09-460-384-37	Sequence 37, Appl
127	6	1.5	137	4	US-09-205-258-310	Sequence 310, App	200	6	1.5	220	3	US-08-463-682-23	Sequence 23, Appl
128	6	1.5	137	4	US-09-904-615-163	Sequence 163, App	201	6	1.5	220	3	US-08-328-208A-21	Sequence 21, Appl
129	6	1.5	137	4	US-09-489-039A-7478	Sequence 7478, Ap	202	6	1.5	220	4	US-08-328-352-8161	Sequence 8161, Ap
130	6	1.5	139	4	US-09-489-039A-8585	Sequence 8585, Ap	203	6	1.5	223	1	US-08-459-818-25	Sequence 25, Appl
131	6	1.5	140	4	US-09-252-991A-21731	Sequence 21731, A	204	6	1.5	223	2	US-08-899-666-25	Sequence 25, Appl
132	6	1.5	141	4	US-08-107-532A-4857	Sequence 4857, Ap	205	6	1.5	223	2	US-08-463-682-25	Sequence 25, Appl
133	6	1.5	143	4	US-08-936-165A-445	Sequence 445, App	206	6	1.5	223	2	US-08-725-776-25	Sequence 25, Appl
134	6	1.5	144	4	US-08-936-165A-445	Sequence 445, App	207	6	1.5	223	2	US-08-463-682-25	Sequence 25, Appl
135	6	1.5	144	4	US-09-252-991A-30783	Sequence 30783, A	208	6	1.5	223	2	US-08-488-062-25	Sequence 25, Appl
136	6	1.5	144	4	US-09-134-000C-6439	Sequence 6439, Ap	209	6	1.5	224	4	US-09-489-039A-9953	Sequence 9953, Ap
137	6	1.5	144	4	US-08-621-976-5120	Sequence 5120, Ap	210	6	1.5	224	4	US-09-543-881A-4654	Sequence 4654, Ap
138	6	1.5	147	4	US-09-328-352-7278	Sequence 7278, Ap	211	6	1.5	225	3	US-08-463-682-23	Sequence 23, Appl
139	6	1.5	147	4	US-09-328-352-7654	Sequence 7654, Ap	212	6	1.5	226	3	US-08-347-594A-4	Sequence 4, Appli
140	6	1.5	147	4	US-09-107-532A-7081	Sequence 7081, Ap	213	6	1.5	226	3	US-08-463-682-5	Sequence 5, Appli
141	6	1.5	149	4	US-09-134-001C-3012	Sequence 3012, Ap	214	6	1.5	227	4	US-09-489-039A-11549	Sequence 11549, A
142	6	1.5	149	4	US-09-328-352-4810	Sequence 4810, Ap	215	6	1.5	234	4	US-09-149-476-353	Sequence 353, App
143	6	1.5	150	3	US-08-052-877-2	Sequence 2, Appli	216	6	1.5	244	4	US-08-328-352-7410	Sequence 7410, Ap
144	6	1.5	150	4	US-09-709-790-2	Sequence 2, Appli	217	6	1.5	245	4	US-09-252-991A-30119	Sequence 30119, A
145	6	1.5	151	4	US-08-134-000C-5616	Sequence 5616, Ap	218	6	1.5	247	2	US-08-797-689-4	Sequence 4, Appli
146	6	1.5	156	4	US-09-252-991A-20612	Sequence 20612, A	219	6	1.5	247	4	US-09-252-991A-32109	Sequence 32109, A
147	6	1.5	158	4	US-09-252-991A-18463	Sequence 18463, A	220	6	1.5	247	4	US-09-134-000C-5239	Sequence 5239, Ap
148	6	1.5	158	4	US-08-808-701A-20	Sequence 20, Appl	221	6	1.5	255	4	US-09-984-186-4	Sequence 4, Appli
149	6	1.5	159	4	US-08-311-731A-85	Sequence 85, Appl	222	6	1.5	255	4	US-09-205-258-385	Sequence 385, App
150	6	1.5	160	2	US-08-602-941-1	Sequence 1, Appli	223	6	1.5	255	4	US-09-252-991A-21286	Sequence 21286, A
151	6	1.5	160	3	US-08-961-364-1	Sequence 1, Appli	224	6	1.5	257	4	US-09-634-238-353	Sequence 353, App
152	6	1.5	160	4	US-08-432-098A-1	Sequence 1, Appli	225	6	1.5	258	4	US-09-396-840-3	Sequence 3, Appli
153	6	1.5	160	4	US-08-612-342-1	Sequence 1, Appli	226	6	1.5	262	3	US-08-961-083-30	Sequence 30, Appl
154	6	1.5	160	4	US-08-612-421A-1	Sequence 1, Appli	227	6	1.5	262	4	US-09-252-991A-32484	Sequence 32484, A
155	6	1.5	160	4	US-09-724-401-1	Sequence 388, App	228	6	1.5	262	4	US-09-536-784-30	Sequence 30, Appl
156	6	1.5	161	4	US-09-615-192A-388	Sequence 388, App	229	6	1.5	265	4	US-09-543-881A-6305	Sequence 6305, Ap
157	6	1.5	163	4	US-09-134-000C-3710	Sequence 3710, Ap	230	6	1.5	266	4	US-09-543-881A-4276	Sequence 4276, Ap
158	6	1.5	171	4	US-09-198-452A-1184	Sequence 1184, Ap	231	6	1.5	268	1	US-08-446-919A-2	Sequence 2, Appli
159	6	1.5	174	4	US-09-149-476-526	Sequence 526, App	232	6	1.5	268	1	US-08-611-880-2	Sequence 2, Appli
160	6	1.5	180	4	US-09-544-716-19	Sequence 19, Appl	233	6	1.5	268	3	US-08-904-284-7	Sequence 7, Appli
161	6	1.5	180	4	US-09-557-921-20	Sequence 20, Appl	234	6	1.5	273	4	US-09-540-236-2730	Sequence 2730, Ap
162	6	1.5	180	4	US-09-619-380-21	Sequence 21, Appl	235	6	1.5	275	4	US-09-252-991A-19583	Sequence 19583, A
163	6	1.5	184	4	US-08-134-001C-4555	Sequence 4555, Ap	236	6	1.5	276	4	US-08-540-236-2404	Sequence 2404, Ap
164	6	1.5	184	4	US-08-134-000C-3779	Sequence 3779, Ap	237	6	1.5	276	4	US-09-155-185-2	Sequence 2, Appli
165	6	1.5	185	1	US-07-988-273-2	Sequence 2, Appli	238	6	1.5	276	4	US-09-328-352-129	Sequence 129, App
166	6	1.5	185	3	US-08-848-810-25	Sequence 25, Appl	239	6	1.5	276	4	US-09-733-383-2	Sequence 2, Appli
167	6	1.5	185	3	US-09-164-193-21	Sequence 21, Appl	240	6	1.5	278	3	US-08-522-813-4	Sequence 4, Appli
168	6	1.5	185	4	US-09-221-448A-21	Sequence 21, Appl	241	6	1.5	278	4	US-09-252-991A-21844	Sequence 21844, A
169	6	1.5	185	5	PCT-US93-12019-2	Sequence 2, Appli	242	6	1.5	279	4	US-09-328-352-5958	Sequence 5958, Ap
170	6	1.5	186	4	US-09-198-452A-915	Sequence 915, App	243	6	1.5	280	4	US-09-252-991A-16878	Sequence 16878, A
171	6	1.5	187	3	US-08-463-682-1	Sequence 1, Appli	244	6	1.5	282	4	US-09-134-001C-3155	Sequence 3155, Ap
172	6	1.5	188	4	US-09-252-991A-20575	Sequence 20575, A	245	6	1.5	282	4	US-09-489-039A-11576	Sequence 11576, A
173	6	1.5	192	1	US-08-848-810-332-4	Sequence 4, Appli	246	6	1.5	284	2	US-08-538-960-2	Sequence 2, Appli

247	6	1.5	285	4	US-09-489-039A-7446	Sequence 7446, Ap	320	6	1.5	343	1	US-08-187-793-2	Sequence 2, Appli
248	6	1.5	286	3	US-08-818-113-81	Sequence 81, Appl	321	6	1.5	343	4	US-09-328-352-6094	Sequence 6094, Ap
249	6	1.5	286	4	US-09-355-166-9	Sequence 9, Appl	322	6	1.5	344	4	US-09-489-039A-13987	Sequence 13987, A
250	6	1.5	286	4	US-08-818-111-82	Sequence 82, Appl	323	6	1.5	348	1	US-08-366-953A-45	Sequence 45, Appl
251	6	1.5	286	4	US-09-056-556-81	Sequence 81, Appl	324	6	1.5	348	2	US-08-484-397A-2	Sequence 2, Appli
252	6	1.5	286	4	US-09-072-596-82	Sequence 82, Appl	325	6	1.5	348	2	US-08-484-397A-3	Sequence 3, Appli
253	6	1.5	286	4	US-09-252-991A-27746	Sequence 27746, A	326	6	1.5	348	2	US-08-484-397A-4	Sequence 4, Appli
254	6	1.5	286	4	US-09-072-967-81	Sequence 81, Appl	327	6	1.5	348	2	US-08-484-397A-5	Sequence 5, Appli
255	6	1.5	287	4	US-09-252-991A-17868	Sequence 17868, A	328	6	1.5	348	2	US-08-484-397A-6	Sequence 6, Appli
256	6	1.5	290	4	US-09-358-383C-8	Sequence 8, Appli	329	6	1.5	348	2	US-08-484-397A-7	Sequence 7, Appli
257	6	1.5	290	4	US-09-543-681A-6454	Sequence 6454, Ap	330	6	1.5	348	2	US-08-484-397A-27	Sequence 27, Appl
258	6	1.5	293	1	US-08-446-925-5	Sequence 5, Appli	331	6	1.5	348	2	US-08-484-397A-38	Sequence 38, Appl
259	6	1.5	293	2	US-09-146-331-5	Sequence 5, Appli	332	6	1.5	350	4	US-09-543-681A-8316	Sequence 8316, Ap
260	6	1.5	293	2	US-08-896-885-5	Sequence 5, Appli	333	6	1.5	351	3	US-08-466-465-6	Sequence 6, Appli
261	6	1.5	293	4	US-09-375-256-5	Sequence 5, Appli	334	6	1.5	353	3	US-09-461-474-4	Sequence 4, Appli
262	6	1.5	293	4	US-09-561-756-21	Sequence 21, Appl	335	6	1.5	353	4	US-09-252-991A-30398	Sequence 30398, A
263	6	1.5	293	4	US-09-227-721-31	Sequence 31, Appl	336	6	1.5	356	4	US-09-252-991A-21259	Sequence 21259, A
264	6	1.5	293	4	US-08-983-502-21	Sequence 21, Appl	337	6	1.5	357	4	US-09-252-991A-20860	Sequence 20860, A
265	6	1.5	293	4	US-09-376-156-5	Sequence 5, Appli	338	6	1.5	359	1	US-07-881-075-2	Sequence 2, Appli
266	6	1.5	293	4	US-08-724-378D-6	Sequence 6, Appli	339	6	1.5	359	1	US-08-120-827-2	Sequence 2, Appli
267	6	1.5	293	4	US-09-516-747-31	Sequence 31, Appl	340	6	1.5	359	1	US-08-478-675-2	Sequence 2, Appli
268	6	1.5	293	4	US-09-954-697-21	Sequence 21, Appl	341	6	1.5	361	4	US-09-328-352-5459	Sequence 5459, Ap
269	6	1.5	293	4	US-09-489-039A-8978	Sequence 8978, Ap	342	6	1.5	363	4	US-09-205-258-553	Sequence 553, App
270	6	1.5	293	5	PCT-US96-10521-31	Sequence 31, Appl	343	6	1.5	370	1	US-08-118-370-18	Sequence 18, Appl
271	6	1.5	294	4	US-09-252-991A-29464	Sequence 29464, A	344	6	1.5	370	5	PCT-US93-08528-18	Sequence 18, Appl
272	6	1.5	295	4	US-09-328-174A-3	Sequence 3, Appli	345	6	1.5	372	4	US-09-252-991A-18963	Sequence 18963, A
273	6	1.5	295	4	US-09-328-352-5392	Sequence 5392, Ap	346	6	1.5	373	3	US-09-039-198A-14	Sequence 14, Appl
274	6	1.5	296	4	US-09-489-039A-7531	Sequence 7531, Ap	347	6	1.5	373	3	US-09-039-198A-15	Sequence 15, Appl
275	6	1.5	296	4	US-09-489-039A-14102	Sequence 14102, A	348	6	1.5	373	4	US-08-877-599-14	Sequence 14, Appl
276	6	1.5	296	3	US-09-080-044-9	Sequence 9, Appli	349	6	1.5	373	4	US-08-877-599-15	Sequence 15, Appl
277	6	1.5	298	4	US-09-531-857A-9	Sequence 9, Appli	350	6	1.5	373	4	US-09-267-574-14	Sequence 14, Appl
278	6	1.5	298	4	US-09-543-681A-6110	Sequence 6110, Ap	351	6	1.5	373	4	US-09-267-574-15	Sequence 15, Appl
279	6	1.5	301	4	US-09-328-352-6885	Sequence 6885, Ap	352	6	1.5	375	1	US-08-205-719-2	Sequence 2, Appli
280	6	1.5	302	4	US-08-957-351-3	Sequence 3, Appli	353	6	1.5	375	3	US-08-746-883-5	Sequence 5, Appli
281	6	1.5	302	4	US-08-957-351-7	Sequence 7, Appli	354	6	1.5	375	4	US-09-573-906-2	Sequence 2, Appli
282	6	1.5	302	4	US-08-957-351-30	Sequence 30, Appl	355	6	1.5	375	4	US-09-252-991A-27411	Sequence 27411, A
283	6	1.5	302	4	US-08-426-630-40	Sequence 40, Appl	356	6	1.5	375	4	US-09-313-177-5	Sequence 5, Appli
284	6	1.5	304	4	US-09-609-816-5	Sequence 5, Appli	357	6	1.5	376	2	US-08-709-923-4	Sequence 4, Appli
285	6	1.5	304	4	US-09-107-532A-7041	Sequence 7041, Ap	358	6	1.5	378	4	US-09-789-300A-4	Sequence 4, Appli
286	6	1.5	304	4	US-09-489-039A-11956	Sequence 11956, A	359	6	1.5	380	3	US-08-857-076-110	Sequence 110, App
287	6	1.5	305	4	US-09-107-532A-5486	Sequence 5486, Ap	360	6	1.5	382	4	US-09-057-996-17	Sequence 17, Appl
288	6	1.5	306	4	US-09-252-991A-23169	Sequence 23169, A	361	6	1.5	383	4	US-09-328-352-5969	Sequence 5969, Ap
289	6	1.5	308	4	US-08-913-816C-17	Sequence 17, Appl	362	6	1.5	383	4	US-09-543-681A-4380	Sequence 4380, Ap
290	6	1.5	309	4	US-09-134-001C-3039	Sequence 3039, Ap	363	6	1.5	386	4	US-09-328-352-7130	Sequence 7130, Ap
291	6	1.5	311	3	US-08-961-083-184	Sequence 184, App	364	6	1.5	387	2	US-08-486-839-6	Sequence 6, Appli
292	6	1.5	311	4	US-09-328-352-6665	Sequence 6665, Ap	365	6	1.5	387	3	US-09-151-011-6	Sequence 6, Appli
293	6	1.5	311	4	US-09-536-784-184	Sequence 184, App	366	6	1.5	387	4	US-09-343-623-6	Sequence 6, Appli
294	6	1.5	312	4	US-09-252-991A-31853	Sequence 31853, A	367	6	1.5	388	4	US-09-880-137-5	Sequence 5, Appli
295	6	1.5	312	4	US-08-957-351-9	Sequence 9, Appli	368	6	1.5	388	4	US-09-880-137-6	Sequence 6, Appli
296	6	1.5	313	4	US-09-198-452A-205	Sequence 205, App	369	6	1.5	389	4	US-09-788-657-23	Patent No. 5240849
297	6	1.5	313	4	US-09-134-000C-6101	Sequence 6101, Ap	370	6	1.5	389	4	US-09-679-279-5	Sequence 5, Appli
298	6	1.5	314	4	US-09-252-991A-27537	Sequence 27537, A	371	6	1.5	390	4	US-09-107-532A-6425	Sequence 6425, Ap
299	6	1.5	318	4	US-09-134-001C-5509	Sequence 5509, Ap	372	6	1.5	392	4	US-09-252-991A-27814	Sequence 27814, A
300	6	1.5	320	2	US-07-841-591A-15	Sequence 15, Appl	373	6	1.5	395	4	US-08-635-552A-4	Sequence 4, Appli
301	6	1.5	320	5	PCT-US93-02034-15	Sequence 15, Appl	374	6	1.5	396	4	US-09-198-452A-147	Sequence 147, App
302	6	1.5	321	2	US-08-592-126-143	Sequence 143, App	375	6	1.5	397	4	US-09-252-991A-20668	Sequence 20668, A
303	6	1.5	321	3	US-08-748-506-10	Sequence 10, Appl	376	6	1.5	398	4	US-09-360-545-20	Sequence 20, Appl
304	6	1.5	321	3	US-08-748-506-18	Sequence 18, Appl	377	6	1.5	398	4	US-09-489-039A-10613	Sequence 10613, A
305	6	1.5	321	4	US-09-168-595-143	Sequence 143, App	378	6	1.5	399	4	US-09-649-747A-11	Sequence 11, Appl
306	6	1.5	322	4	US-09-252-991A-24470	Sequence 24470, A	379	6	1.5	399	4	US-09-649-747A-19	Sequence 19, Appl
307	6	1.5	323	4	US-09-543-681A-5244	Sequence 5244, Ap	380	6	1.5	399	4	US-09-134-000C-5298	Sequence 5298, Ap
308	6	1.5	324	4	US-09-134-001C-5525	Sequence 5525, Ap	381	6	1.5	401	2	US-08-839-008-5	Sequence 5, Appli
309	6	1.5	326	4	US-09-489-039A-7270	Sequence 7270, Ap	382	6	1.5	402	4	US-09-252-991A-22651	Sequence 22651, A
310	6	1.5	328	4	US-09-252-991A-30302	Sequence 30302, A	383	6	1.5	406	4	US-09-252-991A-20043	Sequence 20043, A
311	6	1.5	331	4	US-09-252-991A-24420	Sequence 24420, A	384	6	1.5	410	4	US-09-252-991A-19675	Sequence 19675, A
312	6	1.5	332	4	US-09-107-532A-5821	Sequence 5821, Ap	385	6	1.5	412	4	US-09-554-998A-2	Sequence 2, Appli
313	6	1.5	333	3	US-08-960-780-44	Sequence 44, Appl	386	6	1.5	414	1	US-09-337-913-1	Sequence 1, Appli
314	6	1.5	333	3	US-09-073-898-44	Sequence 44, Appl	387	6	1.5	414	2	US-08-750-524-1	Sequence 1, Appli
315	6	1.5	334	4	US-09-850-351A-48	Sequence 48, Appl	388	6	1.5	414	4	US-09-107-532A-7057	Sequence 7057, Ap
316	6	1.5	334	2	US-08-484-397A-8	Sequence 8, Appli	389	6	1.5	419	2	US-08-270-581-2	Sequence 2, Appli
317	6	1.5	336	2	US-08-665-647-3	Sequence 3, Appli	390	6	1.5	419	4	US-09-146-893-2	Sequence 2, Appli
318	6	1.5	336	4	US-09-107-532A-6417	Sequence 6417, Ap	391	6	1.5	419	4	US-08-675-499A-5	Sequence 5, Appli
319	6	1.5	340	4	US-09-543-681A-7850	Sequence 7850, Ap	392	6	1.5	419	4		

393	6	1.5	419	4	US-08-812-008-5	Sequence 5, Appli	466	6	1.5	494	1	US-08-110-011A-14	Sequence 14, Appl
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395	6	1.5	420	3	US-08-847-065-19	Sequence 19, Appl	468	6	1.5	497	1	US-08-009-075-4	Sequence 4, Appli
396	6	1.5	420	4	US-09-168-595-142	Sequence 142, App	469	6	1.5	498	1	US-08-009-075-5	Sequence 5, Appli
397	6	1.5	421	4	US-09-252-991A-17417	Sequence 17417, A	470	6	1.5	499	4	US-09-134-000C-6426	Sequence 6426, Ap
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399	6	1.5	424	2	US-08-951-148-9	Sequence 9, Appli	472	6	1.5	502	4	US-09-328-352-6568	Sequence 6568, Ap
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401	6	1.5	424	3	US-09-274-570-9	Sequence 9, Appli	474	6	1.5	513	2	US-08-406-855A-21	Sequence 21, Appl
402	6	1.5	425	2	US-08-561-148-3	Sequence 3, Appli	475	6	1.5	513	3	US-09-206-899-21	Sequence 21, Appl
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404	6	1.5	425	3	US-09-274-570-3	Sequence 3, Appli	477	6	1.5	513	4	US-09-592-037-6	Sequence 6, Appli
405	6	1.5	425	4	US-09-489-039A-9445	Sequence 9445, Ap	478	6	1.5	513	4	US-09-428-156B-6	Sequence 6, Appli
406	6	1.5	428	4	US-09-345-236B-62	Sequence 62, Appl	479	6	1.5	515	1	US-08-444-734A-7	Sequence 7, Appli
407	6	1.5	430	4	US-09-352-991A-29055	Sequence 29055, A	480	6	1.5	515	1	US-08-444-734A-7	Sequence 7, Appli
408	6	1.5	433	4	US-09-352-991A-27724	Sequence 27724, A	481	6	1.5	515	1	US-08-444-734A-7	Sequence 7, Appli
409	6	1.5	434	3	US-08-725-459B-42	Sequence 42, Appl	482	6	1.5	515	2	US-08-406-855A-22	Sequence 22, Appl
410	6	1.5	435	4	US-09-491-577-54	Sequence 54, Appl	483	6	1.5	515	3	US-09-206-899-22	Sequence 22, Appl
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412	6	1.5	439	3	US-09-413-814-13	Sequence 13, Appl	485	6	1.5	515	4	US-09-688-415-9	Sequence 9, Appli
413	6	1.5	439	4	US-09-129-668-6	Sequence 6, Appli	486	6	1.5	515	4	US-09-688-415-10	Sequence 10, Appl
414	6	1.5	441	4	US-09-254-776B-79	Sequence 79, Appl	487	6	1.5	515	4	US-09-170-496D-104	Sequence 104, App
415	6	1.5	441	4	US-09-543-681A-7207	Sequence 7207, Ap	488	6	1.5	515	4	US-09-170-496D-220	Sequence 220, App
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419	6	1.5	446	2	US-08-574-138-6	Sequence 6, Appli	492	6	1.5	525	1	US-08-348-891A-2	Sequence 2, Appli
420	6	1.5	446	3	US-08-879-941-2	Sequence 2, Appli	493	6	1.5	525	2	US-08-905-817-2	Sequence 2, Appli
421	6	1.5	446	3	US-09-457-046B-74	Sequence 74, Appl	494	6	1.5	525	4	US-09-252-991A-22536	Sequence 22536, A
422	6	1.5	446	4	US-09-747-116-2	Sequence 2, Appli	495	6	1.5	525	4	US-09-328-352-4897	Sequence 4897, Ap
423	6	1.5	446	4	US-09-761-716-2	Sequence 2, Appli	496	6	1.5	525	4	US-09-540-236-1950	Sequence 1950, Ap
424	6	1.5	451	4	US-09-342-647-10	Sequence 10, Appl	497	6	1.5	530	1	US-08-187-793-4	Sequence 4, Appli
425	6	1.5	454	1	US-08-420-235B-33	Sequence 33, Appl	498	6	1.5	530	4	US-09-252-991A-18090	Sequence 18090, A
426	6	1.5	454	3	US-06-793-624-33	Sequence 33, Appl	499	6	1.5	530	4	US-09-252-991A-23983	Sequence 23983, A
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430	6	1.5	460	4	US-09-328-352-5062	Sequence 5062, Ap							
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436	6	1.5	466	3	US-09-039-198A-4	Sequence 4, Appli							
437	6	1.5	466	4	US-09-343-623-4	Sequence 4, Appli							
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442	6	1.5	468	2	US-08-839-008-7	Sequence 7, Appli							
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445	6	1.5	471	2	US-08-477-451-20	Sequence 20, Appl							
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459	6	1.5	488	3	US-08-477-346-60	Sequence 60, Appl							
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461	6	1.5	488	4	US-08-487-072A-60	Sequence 60, Appl							
462	6	1.5	493	4	US-09-252-991A-26260	Sequence 26260, A							
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464	6	1.5	494	1	US-08-014-723-14	Sequence 14, Appl							
465	6	1.5	494	1	US-08-014-723-16	Sequence 16, Appl							

ALIGNMENTS

RESULT 1

US-09-621-976-3917  
; Sequence 3917, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 3917  
; LENGTH: 151  
; TYPE: PR1  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: -19..-1  
US-09-621-976-3917

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Best Local Similarity 100.0%; Pred.No. 5.6e-144;

Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MEGESTSAVLGCVLALAFQHLNLTDSDTGFLGKGVKGEAKNSITDSQMDVWVYITD 60

Qy 61 IKQYPCYOLFVFNSSGSEVNEQALKILSNVKNVGVYFRHRSQIMTFRRLLHKN 120

Db 61 IQKVPYQVLFYNSGEVNEQAKKILSNVKNVGVYKFRHRSDQIMFRERLLHKN 120  
QY 121 LOEHFSNODLVFLLLTPSIITSCSTHRLH 151  
Db 121 LOEHFSNODLVFLLLTPSIITSCSTHRLH 151

RESULT 2  
US-09-543-681A-6080  
; Sequence 6080, Application US/09543681A  
; Patent No. 6605709  
; GENERAL INFORMATION:  
; APPLICANT: GARY BRETON  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
; FILE REFERENCE: 2709.1002-001  
; CURRENT APPLICATION NUMBER: US/09/543,681A  
; PRIOR FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/128,706  
; PRIOR FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 8344  
; SEQ ID NO 6080  
; LENGTH: 105  
; TYPE: PRT  
; ORGANISM: Proteus mirabilis  
US-09-543-681A-6080

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Best Local Similarity 100.0%; Pred. No. 36;  
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QY 135 LTPSIIT 141  
Db 30 LTPSIIT 36

RESULT 3  
US-09-328-352-5992  
; Sequence 5992, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; PRIOR FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 5992  
; LENGTH: 111  
; TYPE: PRT  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-5992

Query Match 1.7%; Score 7; DB 4; Length 111;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 135 LTPSIIT 141  
Db 34 LTPSIIT 40

RESULT 4  
US-09-621-976-4623  
; Sequence 4623, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2

Db 386 SSPETDE 392  
Db 61 SSPETDE 67

RESULT 5  
US-09-453-195A-4  
; Sequence 4, Application US/09453195A  
; Patent No. 6368826  
; GENERAL INFORMATION:  
; APPLICANT: Ligensa, Tanja  
; APPLICANT: Schumacher, Ralf  
; APPLICANT: Weidner, Michael  
; TITLE OF INVENTION: IGF-1 Receptor Interacting Proteins  
; FILE REFERENCE: 09/453,195  
; CURRENT APPLICATION NUMBER: US/09/453,195A  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: EPO 98122992.5  
; PRIOR FILING DATE: 1998-12-03  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 126  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Xaa at position 123 is any one of the twenty naturally occurring  
US-09-453-195A-4

Query Match 1.7%; Score 7; DB 4; Length 126;  
Best Local Similarity 100.0%; Pred. No. 42;  
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QY 386 SSPETDE 392  
Db 61 SSPETDE 67

RESULT 6  
US-09-446-504-34  
; Sequence 34, Application US/09446504  
; Patent No. 6218150  
; GENERAL INFORMATION:  
; APPLICANT: UEMORI, Takashi  
; APPLICANT: SATO, Yoshimi  
; APPLICANT: FUJITA, Tomoko  
; APPLICANT: MIYAKE, Kazue  
; APPLICANT: MUKAI, Hiroyuki

Db 386 SSPETDE 392  
Db 61 SSPETDE 67

RESULT 6  
US-09-446-504-34  
; Sequence 34, Application US/09446504  
; Patent No. 6218150  
; GENERAL INFORMATION:  
; APPLICANT: UEMORI, Takashi  
; APPLICANT: SATO, Yoshimi  
; APPLICANT: FUJITA, Tomoko  
; APPLICANT: MIYAKE, Kazue  
; APPLICANT: MUKAI, Hiroyuki

; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 4623  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 35  
; OTHER INFORMATION: Xaa = \* ,Tip  
; NAME/KEY: UNSURE  
; LOCATION: 48  
; OTHER INFORMATION: Xaa = Ala,Pro  
; NAME/KEY: UNSURE  
; LOCATION: 36  
; OTHER INFORMATION: Xaa = Asp,His  
US-09-621-976-4623

Query Match 1.7%; Score 7; DB 4; Length 117;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 ERLHKN 120  
Db 19 ERLHKN 25

RESULT 5  
US-09-453-195A-4  
; Sequence 4, Application US/09453195A  
; Patent No. 6368826  
; GENERAL INFORMATION:  
; APPLICANT: Ligensa, Tanja  
; APPLICANT: Schumacher, Ralf  
; APPLICANT: Weidner, Michael  
; TITLE OF INVENTION: IGF-1 Receptor Interacting Proteins  
; FILE REFERENCE: 09/453,195  
; CURRENT APPLICATION NUMBER: US/09/453,195A  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: EPO 98122992.5  
; PRIOR FILING DATE: 1998-12-03  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 126  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Xaa at position 123 is any one of the twenty naturally occurring  
US-09-453-195A-4

Query Match 1.7%; Score 7; DB 4; Length 126;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 386 SSPETDE 392  
Db 61 SSPETDE 67

RESULT 6  
US-09-446-504-34  
; Sequence 34, Application US/09446504  
; Patent No. 6218150  
; GENERAL INFORMATION:  
; APPLICANT: UEMORI, Takashi  
; APPLICANT: SATO, Yoshimi  
; APPLICANT: FUJITA, Tomoko  
; APPLICANT: MIYAKE, Kazue  
; APPLICANT: MUKAI, Hiroyuki

Db 386 SSPETDE 392  
Db 61 SSPETDE 67

RESULT 6  
US-09-446-504-34  
; Sequence 34, Application US/09446504  
; Patent No. 6218150  
; GENERAL INFORMATION:  
; APPLICANT: UEMORI, Takashi  
; APPLICANT: SATO, Yoshimi  
; APPLICANT: FUJITA, Tomoko  
; APPLICANT: MIYAKE, Kazue  
; APPLICANT: MUKAI, Hiroyuki

; APPLICANT: ASADA, Kiyozo  
; APPLICANT: KATO, Ikunoshin  
; TITLE OF INVENTION: DNA POLYMERASE-RELATED FACTORS  
; FILE REFERENCE: 1422-408PCT  
; CURRENT APPLICATION NUMBER: US/09/446,504  
; PRIOR FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: PCT/JP98/02845  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: JP 9-187496  
; PRIOR FILING DATE: 1997-06-26  
; PRIOR APPLICATION NUMBER: JP 9-320692  
; PRIOR FILING DATE: 1997-11-27  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 34  
; LENGTH: 137  
; TYPE: PRT  
; ORGANISM: Pyrococcus furiosus  
US-09-446-504-34

Query Match 1.7%; Score 7; DB 3; Length 137;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 392 EEIEKMK 398  
Db 98 EEIEKMK 104  
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RESULT 7  
US-09-712-266-34  
; Sequence 34, Application US/09712266  
; Patent No. 6333158  
; GENERAL INFORMATION:  
; APPLICANT: ASADA, Kiyozo  
; APPLICANT: KATO, Ikunoshin  
; TITLE OF INVENTION: DNA POLYMERASE-RELATED FACTORS  
; FILE REFERENCE: 1422-408PCT  
; CURRENT APPLICATION NUMBER: US/09/712,266  
; PRIOR FILING DATE: 2000-11-15  
; PRIOR APPLICATION NUMBER: US 09/446,504  
; PRIOR FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: PCT/JP98/02845  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: JP 9-187496  
; PRIOR FILING DATE: 1997-06-26  
; PRIOR APPLICATION NUMBER: JP 9-320692  
; PRIOR FILING DATE: 1997-11-27  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 34  
; LENGTH: 137  
; TYPE: PRT  
; ORGANISM: Pyrococcus furiosus  
US-09-712-266-34

Query Match 1.7%; Score 7; DB 4; Length 137;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 98 EEIEKMK 104  
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RESULT 8  
US-09-540-236-2904  
; Sequence 2904, Application US/09540236

; Patent No. 6673910  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATA  
; FILE REFERENCE: 2709.2005-001  
; CURRENT APPLICATION NUMBER: US/09/540,236  
; CURRENT FILING DATE: 2000-04-04  
; NUMBER OF SEQ ID NOS: 3840  
; SEQ ID NO 2904  
; LENGTH: 182  
; TYPE: PRT  
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US-09-540-236-2904

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Best Local Similarity 100.0%; Pred. No. 59;  
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QY 85 LKXILSN 91  
Db 174 LKXILSN 180  
|||||

RESULT 9  
US-08-772-440-2  
; Sequence 2, Application US/08772440  
; Patent No. 6046158  
; GENERAL INFORMATION:  
; APPLICANT: Arizumi, Kiyoshi  
; APPLICANT: Takashima, Akira  
; TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE  
; TITLE OF INVENTION: LECTIN, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/772,440  
; FILING DATE: CONCURRENTLY HERewith  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parker, David L.  
; REGISTRATION NUMBER: 32,165  
; REFERENCE/DOCKET NUMBER: UTXD:493  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 512/418-3000  
; TELEFAX: 512/474-7577  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 244 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-772-440-2

Query Match 1.7%; Score 7; DB 3; Length 244;  
Best Local Similarity 100.0%; Pred. No. 77;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 VLGLALP 20  
Db 63 VLGLALP 69  
|||||

```
RESULT 10
US-07-956-700B-105
; Sequence 105, Application US/07956700B
; Patent No. 5539092
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5539092th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/956,700B
; FILING DATE: 19921002
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5539092thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
US-07-956-700B-105

Query Match 1.7%; Score 7; DB 1; Length 257;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 389 ETDEEIE 395
Db 112 ETDEEIE 118

RESULT 11
US-08-476-537-105
; Sequence 105, Application US/08476537
; Patent No. 5792620
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5792620th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,607
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5792627thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
US-08-476-537-105
```

```
US-08-476-537-105
; Sequence 105, Application US/08485607
; Patent No. 5792627
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5792627th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,607
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5792627thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
US-08-476-537-105

Query Match 1.7%; Score 7; DB 1; Length 257;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 389 ETDEEIE 395
Db 112 ETDEEIE 118

RESULT 12
US-08-485-607-105
; Sequence 105, Application US/08485607
; Patent No. 5792627
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5792627th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,607
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5792627thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
US-08-476-537-105
```

```
; MOLECULE TYPE: Peptide
US-08-485-607-105

Query Match      1.7%; Score 7; DB 1; Length 257;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      389 ETDEIE 395
DB      112 ETDEIE 118

RESULT 13
US-08-475-879-105
; Sequence 105, Application US/08475879
; Patent No. 5972644
; Patent No. 5972644 5786170
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,879
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5972644 5786170thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
US-08-475-879-105

Query Match      1.7%; Score 7; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      389 ETDEIE 395
DB      112 ETDEIE 118

RESULT 14
US-09-433-043B-105
; Sequence 105, Application US/09433043B
; Patent No. 6393342
; GENERAL INFORMATION:
; APPLICANT: HASELKORN, ROBERT
; APPLICANT: GORNICKI, PIOTR

; TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-CoA CARBOXYLASE
; FILE REFERENCE: ARCD:338US
; CURRENT APPLICATION NUMBER: US/09/433,043B
; CURRENT FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 08/475,879
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/956,700
; PRIOR FILING DATE: 1992-10-02
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 105
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-433-043B-105

Query Match      1.7%; Score 7; DB 4; Length 257;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      389 ETDEIE 395
DB      112 ETDEIE 118

RESULT 15
US-07-941-523-23
; Sequence 23, Application US/07941523
; Patent No. 5571718
; GENERAL INFORMATION:
; APPLICANT: Dunn, John J
; APPLICANT: Barbour, Alan G
; TITLE OF INVENTION: Cloning and Expression of Borrelia
; TITLE OF INVENTION: Lipoproteins
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 01730
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/941,523
; FILING DATE: 19920908
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: BNL90-01A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-941-523-23

Query Match      1.7%; Score 7; DB 1; Length 281;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 250 LKREIEK 256  
Db 197 LKREIEK 203

RESULT 16  
US-09-540-236-2036  
; Sequence 2036, Application US/09540236  
; Patent No. 6673910  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR  
; FILE REFERENCE: 2709.2005-001  
; CURRENT APPLICATION NUMBER: US/09/540,236  
; CURRENT FILING DATE: 2000-04-04  
; NUMBER OF SEQ ID NOS: 3840  
; SEQ ID NO 2036  
; LENGTH: 286  
; TYPE: PRT  
; ORGANISM: M.catarrhalis  
US-09-540-236-2036

Query Match 1.7%; Score 7; DB 4; Length 286;  
Best Local Similarity 100.0%; Pred. No. 89;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 338 ASTPQII 344  
Db 194 ASTPQII 200

RESULT 17  
US-08-320-161-11  
; Sequence 11, Application US/08320161  
; Patent No. 5747294  
; GENERAL INFORMATION:  
; APPLICANT: Flavell, Richard A.  
; APPLICANT: Kantor, Fred S.  
; APPLICANT: Barthold, Stephen W.  
; APPLICANT: Fikrig, Erol  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TITLE OF INVENTION: PREVENTION AND DIAGNOSIS OF LYME DISEASE  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 875 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10022-6250  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/320,161  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/682,355  
; FILING DATE:  
; APPLICATION NUMBER: US 538,969  
; FILING DATE: 15-JUN-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 602,551  
; FILING DATE: 26-OCT-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haley Jr., James F.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: YU-100 CIP 2

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 715-0600  
; TELEFAX: (212) 715-0673  
; TELEX: 14-8367  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 296 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-320-161-11

Query Match 1.7%; Score 7; DB 1; Length 296;  
Best Local Similarity 100.0%; Pred. No. 92;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 LKREIEK 256  
Db 212 LKREIEK 218

RESULT 18  
US-08-137-175A-3  
; Sequence 3, Application US/08137175A  
; Patent No. 577095  
; GENERAL INFORMATION:  
; APPLICANT: BARBOUR, Alan G.  
; APPLICANT: BERGSTROM, Sven  
; APPLICANT: HANSSON, Lennart  
; TITLE OF INVENTION: IMPROVEMENT IN BORRELIA BURGDORFERI AND  
; TITLE OF INVENTION: PROPHYLAXIS  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/137,175A  
; FILING DATE: 26-OCT-1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/08972  
; FILING DATE: 22-OCT-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: COOPER, Iver P.  
; REGISTRATION NUMBER: 28,005  
; REFERENCE/DOCKET NUMBER: BARBOUR-1B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 296 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-137-175A-3

Query Match 1.7%; Score 7; DB 1; Length 296;  
Best Local Similarity 100.0%; Pred. No. 92;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 LKREIEK 256  
Db 212 LKREIEK 218



Db 212 LKREIEK 218

RESULT 19

US-08-479-017-3

Sequence 3, Application US/08479017

Patent No. 6143872

GENERAL INFORMATION:

APPLICANT: BARBOUR, Alan G.

APPLICANT: BERGSTROM, Sven

APPLICANT: HANSSON, Lennart

TITLE OF INVENTION: IMPROVEMENT IN BORRELIA BURGDORFERI AND

TITLE OF INVENTION: PROPHYLAXIS

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/479,017

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/137,175

FILING DATE: 26-OCT-1993

APPLICATION NUMBER: PCT/US92/08972

FILING DATE: 22-OCT-1992

ATTORNEY/AGENT INFORMATION:

NAME: COOPER, Iver P.

REGISTRATION NUMBER: 28,005

REFERENCE/DOCKET NUMBER: BARBOUR-1B

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

TELEX: 248633

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 296 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-479-017-3

Query Match 1.7%; Score 7; DB 3; Length 296;

Best Local Similarity 100.0%; Pred. No. 92;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 LKREIEK 256

Db 212 LKREIEK 218

RESULT 20

US-08-455-829-11

Sequence 11, Application US/08455829

Patent No. 6197301

GENERAL INFORMATION:

APPLICANT: Flavell, Richard A.

APPLICANT: Kantox, Fred S.

APPLICANT: Barthold, Stephen W.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

TITLE OF INVENTION: PREVENTION AND DIAGNOSIS OF LYME DISEASE

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brookhaven National Laboratory

STREET:

CITY: Upton

STATE: NY

COUNTRY: USA

ZIP: 11973

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/235,836C

FILING DATE: 29-APR-1994

US-08-235-836C-22

Sequence 22, Application US/08235836C

Patent No. 6248562

GENERAL INFORMATION:

APPLICANT: Dunn, John J.

APPLICANT: Luft, Benjamin J.

TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising

TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor

NUMBER OF SEQUENCES: 144

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brookhaven National Laboratory

STREET:

CITY: Upton

STATE: NY

COUNTRY: USA

ZIP: 11973

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/235,836C

FILING DATE: 29-APR-1994

US-08-455-829-11

Query Match 1.7%; Score 7; DB 3; Length 296;

Best Local Similarity 100.0%; Pred. No. 92;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 LKREIEK 256

Db 212 LKREIEK 218

RESULT 21

US-08-235-836C-22

Sequence 22, Application US/08235836C

Patent No. 6248562

GENERAL INFORMATION:

APPLICANT: Dunn, John J.

APPLICANT: Luft, Benjamin J.

TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising

TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor

NUMBER OF SEQUENCES: 144

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brookhaven National Laboratory

STREET:

CITY: Upton

STATE: NY

COUNTRY: USA

ZIP: 11973

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/235,836C

FILING DATE: 29-APR-1994

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/148,191  
FILING DATE: 01-11-93  
ATTORNEY/AGENT INFORMATION:  
NAME: Bogosian, Margaret C.  
REGISTRATION NUMBER: 25,324  
REFERENCE/DOCKET NUMBER: BNL93-28A  
TELEPHONE: (516) 282-7338  
TELEFAX: (516) 282-3729  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 296 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-235-836C-22

Query Match 1.7%; Score 7; DB 3; Length 296;  
Best Local Similarity 100.0%; Pred. No. 92;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 250 LKREIEK 256  
Db 212 LKREIEK 218

RESULT 22  
US-08-455-973-11  
Sequence 11, Application US/08455973  
Patent No. 6344552  
GENERAL INFORMATION:  
APPLICANT: Flavell, Richard A.  
Kantox, Fred S.  
Barthold, Stephen W.  
Fikrig, Erol  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE PREVENTION AND DIAGNOSIS OF LYME DISEASE  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 875 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10022-6250  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,973  
FILING DATE: 31-May-1995  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/320,161  
FILING DATE: 07-OCT-1994  
APPLICATION NUMBER: <Unknown>  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US/07/682,355  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 538,969  
FILING DATE: 15-JUN-1990  
APPLICATION NUMBER: US 602,551  
FILING DATE: 26-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: YU-100 CIP 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 715-0600

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/148,191  
FILING DATE: 01-11-93  
ATTORNEY/AGENT INFORMATION:  
NAME: Bogosian, Margaret C.  
REGISTRATION NUMBER: 25,324  
REFERENCE/DOCKET NUMBER: BNL93-28A  
TELEPHONE: (516) 282-7338  
TELEFAX: (516) 282-3729  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 296 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-235-836C-22

Query Match 1.7%; Score 7; DB 3; Length 296;  
Best Local Similarity 100.0%; Pred. No. 92;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 250 LKREIEK 256  
Db 212 LKREIEK 218

RESULT 22  
US-08-455-973-11  
Sequence 11, Application US/08455973  
Patent No. 6344552  
GENERAL INFORMATION:  
APPLICANT: Flavell, Richard A.  
Kantox, Fred S.  
Barthold, Stephen W.  
Fikrig, Erol  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE PREVENTION AND DIAGNOSIS OF LYME DISEASE  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 875 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10022-6250  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,973  
FILING DATE: 31-May-1995  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/320,161  
FILING DATE: 07-OCT-1994  
APPLICATION NUMBER: <Unknown>  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US/07/682,355  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 538,969  
FILING DATE: 15-JUN-1990  
APPLICATION NUMBER: US 602,551  
FILING DATE: 26-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: YU-100 CIP 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 715-0600

TELEFAX: (212) 715-0673  
TELEX: 14-8367  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 296 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-08-455-973-11

Query Match 1.7%; Score 7; DB 4; Length 296;  
Best Local Similarity 100.0%; Pred. No. 92;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 250 LKREIEK 256  
Db 212 LKREIEK 218

RESULT 23  
US-09-910-174B-12  
Sequence 12, Application US/09910174B  
Patent No. 6630575  
GENERAL INFORMATION:  
APPLICANT: Coyle, Anthony J.  
APPLICANT: Fraser, Christopher C.  
APPLICANT: Manning, Stephen  
TITLE OF INVENTION: B7-H2 Molecules, No. 6630575el Members of the B7  
FILE OF INVENTION: Family and Uses Thereof  
FILE REFERENCE: 35800/236924  
CURRENT APPLICATION NUMBER: US/09/910,174B  
CURRENT FILING DATE: 2001-07-20  
PRIOR APPLICATION NUMBER: US 09/620,461  
PRIOR FILING DATE: 2000-07-20  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12  
LENGTH: 319  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-910-174B-12

Query Match 1.7%; Score 7; DB 4; Length 319;  
Best Local Similarity 100.0%; Pred. No. 99;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 221 SQEELK 227  
Db 307 SQEELK 313

RESULT 24  
US-09-620-461-12  
Sequence 12, Application US/09620461  
Patent No. 6635750  
GENERAL INFORMATION:  
APPLICANT: Coyle, Anthony J.  
APPLICANT: Fraser, Christopher C.  
APPLICANT: Manning, Stephen  
TITLE OF INVENTION: B7-H2 Molecules, No. 6635750el Members of the B7  
FILE OF INVENTION: Family and Uses Thereof  
FILE REFERENCE: 5800-149  
CURRENT APPLICATION NUMBER: US/09/620,461  
CURRENT FILING DATE: 2000-07-20  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 12  
LENGTH: 319  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-620-461-12

Query Match 1.7%; Score 7; DB 4; Length 319;  
Best Local Similarity 100.0%; Pred. No. 99;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 221 SLOEELK 227  
DB 307 SLOEELK 313

RESULT 25  
US-08-748-506-13  
Sequence 13, Application US/08748506  
Patent No. 6159707  
GENERAL INFORMATION:  
APPLICANT: Rohnett et al.  
TITLE OF INVENTION: NOVEL SPERM RECEPTORS  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Leydig, Voit & Mayer, Ltd.  
STREET: Two Prudential Plaza, Suite 4900  
CITY: Chicago  
STATE: IL  
COUNTRY: US  
ZIP: 60601-6780  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/748,506  
FILING DATE: 08-NOV-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/033,751  
FILING DATE: 09-NOV-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
REFERENCE/DOCKET NUMBER: 74940  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-616-5600  
TELEFAX: 312-616-5700  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 321 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-748-506-13

Query Match 1.7%; Score 7; DB 3; Length 321;  
Best Local Similarity 100.0%; Pred. No. 99;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 ALKKILS 90  
DB 312 ALKKILS 318

RESULT 26  
US-08-724-394A-6  
Sequence 6, Application US/08724394A  
Patent No. 5872237  
GENERAL INFORMATION:  
APPLICANT: Feder, John N.  
APPLICANT: Kronmal, Gregory S.  
APPLICANT: Lauer, Peter M.  
APPLICANT: Ruddy, David A.  
APPLICANT: Thomas, Winston  
APPLICANT: Tsuchihashi, Zenta  
APPLICANT: Wolff, Roger K.  
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el

TITLE OF INVENTION: Sequences and Antibodies Thereto  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/724,394A  
FILING DATE: 01-OCT-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Pitts, Renee A.  
REGISTRATION NUMBER: 35,136  
REFERENCE/DOCKET NUMBER: C17957-000100  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 342 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..342  
OTHER INFORMATION: /note= "BTF4"  
US-08-724-394A-6

Query Match 1.7%; Score 7; DB 2; Length 342;  
Best Local Similarity 100.0%; Pred. No. 1..1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 221 SLOEELK 227  
DB 330 SLOEELK 336

RESULT 27  
US-09-910-174B-14  
Sequence 14, Application US/09910174B  
Patent No. 6630575  
GENERAL INFORMATION:  
APPLICANT: Coyle, Anthony J.  
APPLICANT: Fraser, Christopher C.  
APPLICANT: Manning, Stephen  
TITLE OF INVENTION: B7-H2 Molecules, No. 6630575al Members of the B7  
FILE REFERENCE: 35800/236924  
CURRENT APPLICATION NUMBER: US/09/910,174B  
CURRENT FILING DATE: 2001-07-20  
PRIOR APPLICATION NUMBER: US 09/620,461  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 14  
LENGTH: 357  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-910-174B-14

Query Match 1.7%; Score 7; DB 4; Length 357;  
Best Local Similarity 100.0%; Pred. No. 1..1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 380 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-235-836C-118

Query Match      1.7%; Score 7; DB 3; Length 380;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      250 LKREIEK 256
Db      196 LKREIEK 202

RESULT 30
US-08-235-836C-114
; Sequence 114, Application US/08235836C
; Patent No. 6248562
; GENERAL INFORMATION:
; APPLICANT: Dunn, John J.
; APPLICANT: Luft, Benjamin J.
; TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
; TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
; NUMBER OF SEQUENCES: 144
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brookhaven National Laboratory
; STREET:
; CITY: Upton
; STATE: NY
; COUNTRY: USA
; ZIP: 11973
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/235,836C
; FILING DATE: 29-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,191
; FILING DATE: 01-11-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Bogosian, Margaret C.
; REGISTRATION NUMBER: 25,324
; REFERENCE/DOCKET NUMBER: BNL93-28A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 282-7338
; TELEFAX: (516) 282-3729
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 393 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-235-836C-114

Query Match      1.7%; Score 7; DB 3; Length 393;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      250 LKREIEK 256
Db      196 LKREIEK 202

RESULT 31
US-09-252-991A-20165
; Sequence 20165, Application US/09252991A
; Patent No. 6551795
; INFORMATION FOR SEQ ID NO: 118:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 380 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-252-991A-20165

Query Match      1.7%; Score 7; DB 4; Length 357;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      221 SLQEELK 227
Db      305 SLQEELK 311

RESULT 28
US-09-620-461-14
; Sequence 14, Application US/09620461
; Patent No. 6635750
; GENERAL INFORMATION:
; APPLICANT: Coyne, Anthony J.
; APPLICANT: Fraser, Christopher C.
; APPLICANT: Manning, Stephen
; TITLE OF INVENTION: B7-H2 Molecules, No. 6635750el Members of the B7
; TITLE OF INVENTION: Family and Uses Thereof
; FILE REFERENCE: 5800-149
; CURRENT APPLICATION NUMBER: US/09/620,461
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-620-461-14

Query Match      1.7%; Score 7; DB 4; Length 357;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      221 SLQEELK 227
Db      305 SLQEELK 311

RESULT 29
US-08-235-836C-118
; Sequence 118, Application US/08235836C
; Patent No. 6248562
; GENERAL INFORMATION:
; APPLICANT: Dunn, John J.
; APPLICANT: Luft, Benjamin J.
; TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
; TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
; NUMBER OF SEQUENCES: 144
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brookhaven National Laboratory
; STREET:
; CITY: Upton
; STATE: NY
; COUNTRY: USA
; ZIP: 11973
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/235,836C
; FILING DATE: 29-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,191
; FILING DATE: 01-11-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Bogosian, Margaret C.
; REGISTRATION NUMBER: 25,324
; REFERENCE/DOCKET NUMBER: BNL93-28A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 282-7338
; TELEFAX: (516) 282-3729
; INFORMATION FOR SEQ ID NO: 118:
```

GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.126  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,798  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 20165  
; LENGTH: 417  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-20165

Query Match 1.7%; Score 7; DB 4; Length 417;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 ASPASTP 341  
|||||||  
Db 369 ASPASTP 375

RESULT 32  
US-08-235-836C-120  
; Sequence 120, Application US/08235836C  
; Patent No. 6248562  
; GENERAL INFORMATION:  
; APPLICANT: Dunn, John J.  
; APPLICANT: Luft, Benjamin J.  
; TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising  
; TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor  
; NUMBER OF SEQUENCES: 144  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brookhaven National Laboratory  
; STREET:  
; CITY: Upton  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 11973

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/235,836C  
; FILING DATE: 29-APR-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/148,191  
; FILING DATE: 01-11-93  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bogosian, Margaret C.  
; REGISTRATION NUMBER: 25,324  
; REFERENCE/DOCKET NUMBER: BNL93-28A  
; TELEPHONE: (516) 282-7338  
; TELEFAX: (516) 282-3729  
; INFORMATION FOR SEQ ID NO: 120:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 441 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-235-836C-120

Query Match 1.7%; Score 7; DB 3; Length 441;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 250 LKREIEK 256  
|||||||  
Db 196 LKREIEK 202

RESULT 33  
US-08-878-989-2  
; Sequence 2, Application US/08879899  
; Patent No. 5885803  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl G.  
; APPLICANT: Lal, Preeti  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Shah, Purvi  
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN  
; TITLE OF INVENTION: KINASES  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/878,989  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0321 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 448 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: TBLYN0T01  
; CLONE: 40194  
US-08-878-989-2

Query Match 1.7%; Score 7; DB 2; Length 448;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 QALKKIL 89  
|||||||  
Db 247 QALKKIL 253

RESULT 34  
US-09-272-796-2  
; Sequence 2, Application US/09272796  
; Patent No. 6207148

GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Corley, Neil C.  
APPLICANT: Guegler, Karl G.  
APPLICANT: Lal, Preeti  
APPLICANT: Goli, Surya K.  
APPLICANT: Shah, Purvi  
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN  
TITLE OF INVENTION: KINASES  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/272,796  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/878,989  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J J  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0321 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 448 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: TELYNOT01  
CLONE: 40194  
US-09-272-796-2  
Query Match 1.7%; Score 7; DB 3; Length 448;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 83 QALKKIL 89  
DB 247 QALKKIL 253  
RESULT 35  
US-08-235-836C-116  
Sequence 116, Application US/08235836C  
Patent No. 6248562  
GENERAL INFORMATION:  
APPLICANT: Dunn, John J.  
APPLICANT: Luft, Benjamin J.  
TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising  
TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor  
NUMBER OF SEQUENCES: 144  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brookhaven National Laboratory  
STREET:  
CITY: Upton  
STATE: NY

COUNTRY: USA  
ZIP: 11973  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/235,836C  
FILING DATE: 29-APR-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/148,191  
FILING DATE: 01-11-93  
ATTORNEY/AGENT INFORMATION:  
NAME: Bogosian, Margaret C.  
REGISTRATION NUMBER: 25,324  
REFERENCE/DOCKET NUMBER: ENL93-28A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 282-7338  
TELEFAX: (516) 282-3729  
INFORMATION FOR SEQ ID NO: 116:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 454 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-235-836C-116  
Query Match 1.7%; Score 7; DB 3; Length 454;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 250 LKREIEK 256  
DB 196 LKREIEK 202  
RESULT 36  
US-09-328-352-4637  
Sequence 4637, Application US/09328352  
Patent No. 6562958  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: GTC99-03PA  
CURRENT APPLICATION NUMBER: US/09/328,352  
CURRENT FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 8252  
SEQ ID NO 4637  
LENGTH: 495  
TYPE: PRT  
ORGANISM: Acinetobacter baumannii  
US-09-328-352-4637  
Query Match 1.7%; Score 7; DB 4; Length 495;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 82 EQALKKI 88  
DB 230 EQALKKI 236  
RESULT 37  
US-09-134-001C-3598  
Sequence 3598, Application US/09134001C  
Patent No. 6380370  
GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 3598  
; LENGTH: 502  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-3598

Query Match 1.7%; Score 7; DB 4; Length 502;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 221 SQBELK 227  
Db 119 SQBELK 125

RESULT 39  
US-09-344-700-4  
; Sequence 4, Application US/09344700  
; Patent No. 6265194  
; GENERAL INFORMATION:  
; APPLICANT: Nezu, Jun-Ichi  
; TITLE OF INVENTION: NOVEL SERINE-THREONINE KINASE GENE  
; FILE REFERENCE: 06501/033001  
; CURRENT APPLICATION NUMBER: US/09/344,700  
; CURRENT FILING DATE: 1999-06-25  
; EARLIER APPLICATION NUMBER: PCT/JP97/0485  
; EARLIER FILING DATE: 1997-12-25  
; EARLIER APPLICATION NUMBER: JP 8-357864  
; EARLIER FILING DATE: 1996-12-27  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 508  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-344-700-4

Query Match 1.7%; Score 7; DB 3; Length 508;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 QALKKIL 89  
Db 307 QALKKIL 313

RESULT 39  
US-09-563-997A-4  
; Sequence 4, Application US/09563997A  
; Patent No. 6674437  
; GENERAL INFORMATION:  
; APPLICANT: Nezu, Jun-Ichi  
; TITLE OF INVENTION: NOVEL SERINE-THREONINE KINASE GENE  
; FILE REFERENCE: 06501-033002  
; CURRENT APPLICATION NUMBER: US/09/563,997A  
; CURRENT FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: US 09/344,700  
; PRIOR FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: PCT/JP97/04855  
; PRIOR FILING DATE: 1997-12-25  
; PRIOR APPLICATION NUMBER: JP 8-357864  
; PRIOR FILING DATE: 1996-12-27  
; NUMBER OF SEQ ID NOS: 48

; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 508  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-563-997A-4

Query Match 1.7%; Score 7; DB 4; Length 508;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 QALKKIL 89  
Db 307 QALKKIL 313

RESULT 40  
US-09-252-991A-16994  
; Sequence 16994, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 16994  
; LENGTH: 522  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-16994

Query Match 1.7%; Score 7; DB 4; Length 522;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 255 EXRGAQ 261  
Db 514 EXRGAQ 520

RESULT 41  
US-09-252-991A-17824  
; Sequence 17824, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 17824  
; LENGTH: 557  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (224)  
; OTHER INFORMATION: Identity of amino acid at the above locations are unknown.  
US-09-252-991A-17824

Query Match 1.7%; Score 7; DB 4; Length 557;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 260 AQIOAAR 266  
| | | | |  
Db 49 AQIOAAR 55

RESULT 42  
US-09-173-053-18  
; Sequence 18, Application US/09173053  
; Patent No. 6451769  
; GENERAL INFORMATION:  
; APPLICANT: HUEBNER, Robert C.  
; APPLICANT: NORMAN, Jon A.  
; APPLICANT: LIANG, Xiaowu  
; APPLICANT: CARNER, Kristin R.  
; APPLICANT: BARBOUR, Alan G.  
; APPLICANT: LUKE, Catherine J.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ADMINISTERING BORRELIA DNA  
; FILE REFERENCE: 454312-2440.1  
; CURRENT APPLICATION NUMBER: US/09/173,053  
; CURRENT FILING DATE: 1998-10-15  
; PRIOR APPLICATION NUMBER: 08/663,998  
; PRIOR FILING DATE: 1996-06-14  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 569  
; TYPE: PRT  
; ORGANISM: Borrelia burgdorferi  
US-09-173-053-18

Query Match 1.7%; Score 7; DB 4; Length 569;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 250 LKREIEK 256  
| | | | |  
Db 485 LKREIEK 491

RESULT 43  
US-08-235-836C-122  
; Sequence 122, Application US/08235836C  
; Patent No. 6248562  
; GENERAL INFORMATION:  
; APPLICANT: Dunn, John J.  
; APPLICANT: Luft, Benjamin J.  
; TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising  
; TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor  
; NUMBER OF SEQUENCES: 144  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brookhaven National Laboratory  
; STREET:  
; CITY: Upton  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 11973  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/235,836C  
; FILING DATE: 29-APR-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/148,191  
; FILING DATE: 01-11-93  
; ATTORNEY/AGENT INFORMATION:

NAME: Bogosian, Margaret C.  
REGISTRATION NUMBER: 25,324  
REFERENCE/DOCKET NUMBER: ENL93-28A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 282-7338  
TELEFAX: (516) 282-3729  
INFORMATION FOR SEQ ID NO: 122:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 588 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-235-836C-122

Query Match 1.7%; Score 7; DB 3; Length 588;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 250 LKREIEK 256  
| | | | |  
Db 196 LKREIEK 202

RESULT 44  
US-09-252-991A-23497  
; Sequence 23497, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 23497  
; LENGTH: 633  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-23497

Query Match 1.7%; Score 7; DB 4; Length 633;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 335 ASPASTP 341  
| | | | |  
Db 82 ASPASTP 88

RESULT 45  
US-09-252-991A-19167  
; Sequence 19167, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 19167  
; LENGTH: 693  
; TYPE: PRT



```
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19167

Query Match      1.7%; Score 7; DB 4; Length 693;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 GFVLGAL 18
DB      671 GFVLGAL 677

RESULT 46
US-09-433-043B-126
; Sequence 126, Application US/09433043B
; Patent No. 6399342
; GENERAL INFORMATION:
; APPLICANT: HASELKORN, ROBERT
; APPLICANT: GORNICKI, PIOTR
; TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-CoA CARBOXYLASE
; FILE REFERENCE: ARCD:338US
; CURRENT APPLICATION NUMBER: US/09/433,043B
; CURRENT FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 08/475,879
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/956,700
; PRIOR FILING DATE: 1992-10-02
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 126
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-433-043B-126

Query Match      1.7%; Score 7; DB 4; Length 694;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      389 ETDEEIE 395
DB      549 ETDEEIE 555

RESULT 47
US-09-910-174B-15
; Sequence 15, Application US/09910174B
; Patent No. 6630575
; GENERAL INFORMATION:
; APPLICANT: Coyle, Anthony J.
; APPLICANT: Fraser, Christopher C.
; APPLICANT: Manning, Stephen
; TITLE OF INVENTION: B7-H2 Molecules, No. 6630575el Members of the B7
; FILE REFERENCE: 35800/236924
; CURRENT APPLICATION NUMBER: US/09/910,174B
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 09/620,461
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 731
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(731)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-910-174B-15

; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19167

Query Match      1.7%; Score 7; DB 4; Length 693;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 GFVLGAL 18
DB      671 GFVLGAL 677

RESULT 46
US-09-433-043B-126
; Sequence 126, Application US/09433043B
; Patent No. 6399342
; GENERAL INFORMATION:
; APPLICANT: HASELKORN, ROBERT
; APPLICANT: GORNICKI, PIOTR
; TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-CoA CARBOXYLASE
; FILE REFERENCE: ARCD:338US
; CURRENT APPLICATION NUMBER: US/09/433,043B
; CURRENT FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 08/475,879
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/956,700
; PRIOR FILING DATE: 1992-10-02
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 126
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-433-043B-126

Query Match      1.7%; Score 7; DB 4; Length 694;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      389 ETDEEIE 395
DB      549 ETDEEIE 555

RESULT 47
US-09-910-174B-15
; Sequence 15, Application US/09910174B
; Patent No. 6630575
; GENERAL INFORMATION:
; APPLICANT: Coyle, Anthony J.
; APPLICANT: Fraser, Christopher C.
; APPLICANT: Manning, Stephen
; TITLE OF INVENTION: B7-H2 Molecules, No. 6630575el Members of the B7
; FILE REFERENCE: 35800/236924
; CURRENT APPLICATION NUMBER: US/09/910,174B
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 09/620,461
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 731
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(731)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-910-174B-15

; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19167

Query Match      1.7%; Score 7; DB 4; Length 731;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      221 SLOEELK 227
DB      310 SLOEELK 316

RESULT 48
US-09-620-461-15
; Sequence 15, Application US/09620461
; Patent No. 6635750
; GENERAL INFORMATION:
; APPLICANT: Coyle, Anthony J.
; APPLICANT: Fraser, Christopher C.
; APPLICANT: Manning, Stephen
; TITLE OF INVENTION: B7-H2 Molecules, No. 6635750el Members of the B7
; FILE REFERENCE: 5800-149
; CURRENT APPLICATION NUMBER: US/09/620,461
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 731
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(731)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-620-461-15

Query Match      1.7%; Score 7; DB 4; Length 731;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      221 SLOEELK 227
DB      310 SLOEELK 316

RESULT 49
US-08-249-380-2
; Sequence 2, Application US/08249380
; Patent No. 5827685
; GENERAL INFORMATION:
; APPLICANT: Lindquist, Susan
; TITLE OF INVENTION: Methods and Compositions of Genetic
; TITLE OF INVENTION: Stress Response Systems
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/249,380
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/710,187
; FILING DATE: 31-MAY-1991
; ATTORNEY/AGENT INFORMATION:
```

NAME: Parker, David L.  
REGISTRATION NUMBER: 32,165  
REFERENCE/DOCKET NUMBER: ARCD:024  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713-787-1400  
TELEFAX: 713-789-2679  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 908 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-249-380-2

Query Match 1.7%; Score 7; DB 2; Length 908;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 ASLQBEL 226  
Db 453 ASLQBEL 459

RESULT 50  
US-09-883-134-4  
Sequence 4, Application US/09883134  
Patent No. 6511840  
GENERAL INFORMATION:  
APPLICANT: Walke, D. Wade  
APPLICANT: Scoville, John  
APPLICANT: Donoho, Gregory  
APPLICANT: Turner, C. Alexander Jr.  
APPLICANT: Mathur, Brian  
APPLICANT: Mathur, Daniel  
APPLICANT: Friddle, Carl Johan  
TITLE OF INVENTION: No. 6511840el Human Kinase Proteins and Polynucleotides Encoding  
FILE REFERENCE: LEX-0193-USA  
CURRENT APPLICATION NUMBER: US/09/883,134  
CURRENT FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: US 60/211,572  
PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: US 60/216,382  
PRIOR FILING DATE: 2000-07-07  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 1236  
TYPE: PRT  
ORGANISM: homo sapiens  
US-09-883-134-4

Query Match 1.7%; Score 7; DB 4; Length 1236;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 QAAREKN 269  
Db 512 QAAREKN 518

RESULT 51  
US-09-181-706-2  
Sequence 2, Application US/09181706  
Patent No. 6130068  
GENERAL INFORMATION:  
APPLICANT: Melanie K. Spriggs, Michael R. Comeau,  
APPLICANT: Robert F. DuBose, Richard S. Johnson  
TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN  
RECEPTOR DNA AND POLYPEPTIDES  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Janis C. Henry

STREET: 51 University St.  
CITY: Seattle  
STATE: WA  
COUNTRY: US  
ZIP: 98101  
COMPUTER READABLE FORM: disk  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/181,706  
FILING DATE: October 28, 1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/958,598 (converted to a  
APPLICATION NUMBER: Provisional, see below)  
FILING DATE: October 28, 1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: --to be assigned-- (USSN 08/958,598  
APPLICATION NUMBER: conversion to Provisional application)  
FILING DATE: October 26, 1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Henry, Janis C  
REGISTRATION NUMBER: 34,347  
REFERENCE/DOCKET NUMBER: 2631-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)470-4189  
TELEFAX: (206)233-0644  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1568 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-181-706-2

Query Match 1.7%; Score 7; DB 3; Length 1568;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 283 ALRTFFP 289  
Db 1022 ALRTFFP 1028

RESULT 52  
US-09-458-791-2  
Sequence 2, Application US/09458791  
Patent No. 6174689  
GENERAL INFORMATION:  
APPLICANT: Spriggs, Melanie  
TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN  
RECEPTOR DNA AND POLYPEPTIDES  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Janis C. Henry  
STREET: 51 University St.  
CITY: Seattle  
STATE: WA  
COUNTRY: US  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: MS-DOS/Windows 95  
SOFTWARE: Word for Windows 95, 7.0a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/458,791  
FILING DATE: 10-Dec-1999  
CLASSIFICATION: <Unknown>

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/958,598
; FILING DATE: 28-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)470-4189
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1568 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-458-791-2

Query Match 1.7%; Score 7; DB 3; Length 1568;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 283 ALRTFFP 289
Db 1022 ALRTFFP 1028

RESULT 53
US-09-459-066-2
; Sequence 2, Application US/09459066
; Patent No. 6187909
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C. Henry
; STREET: 51 University St.
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS/Windows 95
; SOFTWARE: Word for Windows 95, 7.0a
; CURRENT APPLICATION DATA: US/09/459,066
; APPLICATION NUMBER: US/09/459,066
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/958,598
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)470-4189
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1568 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-459-065-2

Query Match 1.7%; Score 7; DB 4; Length 1568;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 283 ALRTFFP 289
Db 1022 ALRTFFP 1028

RESULT 55
US-08-462-128-28
; Sequence 28, Application US/08462128
; Patent No. 5686059
; GENERAL INFORMATION:
; APPLICANT: Goetinck, Paul F.
; APPLICANT: Tondravi, Mehrdad
; TITLE OF INVENTION: CARTILAGE MATRIX PROTEIN AND METHODS FOR
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield
; STREET: 60 State Street
; CITY: Boston

```

```

; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,128
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/006,096
; FILING DATE: 15-JAN-1993
; APPLICATION NUMBER: US 07/866,403
; FILING DATE: 10-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Paul L.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: MGP-005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-462-128-28

Query Match 1.5%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 129 DLVFL 134
Db 1 DLVFL 6

US-08-463-180-28

RESULT 57
US-09-171-705-77
; Sequence 77, Application US/09171705
; Patent No. 6184204
; GENERAL INFORMATION:
; APPLICANT: BOOTS, ANNA M.H.
; APPLICANT: VERHEIJEN, GILBERTUS F.M.
; TITLE OF INVENTION: NOVEL PEPTIDES SUITABLE FOR USE IN ANTIGEN SPECIFIC
; TITLE OF INVENTION: IMMUNOSUPPRESSIVE THERAPY
; FILE REFERENCE: O/96198 US
; CURRENT APPLICATION NUMBER: US/09/171,705
; CURRENT FILING DATE: 1999-02-09
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 77
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DERIVED FROM
; OTHER INFORMATION: SEQUENCE OF HUMAN CARTILAGE (HC) -39 PROTEIN
US-09-171-705-77

Query Match 1.5%; Score 6; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 348 ALDLD 353
Db 3 ALDLD 8

US-08-199-508-57
; Sequence 57, Application US/08199508
; Patent No. 5717058
; GENERAL INFORMATION:
; APPLICANT: Matthews, Maura-Ann H.
; APPLICANT: Stetler, Gary L.
; APPLICANT: Anthony-Cahill, Spencer J.
; APPLICANT: Anderson, David C.
; TITLE OF INVENTION: Modulators of Gene Expression
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Somatogen, Inc.
; STREET: 5797 Central Avenue
; CITY: Boulder
; STATE: Colorado
; ZIP: 80301
; COMPUTER READABLE FORM:

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MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: System 7.0.1  
SOFTWARE: Microsoft Word 5.0a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/199,508  
FILING DATE: February 18, 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/021,536  
FILING DATE: February 23, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5717058ak, Henry P.  
REGISTRATION NUMBER: 33200  
REFERENCE/DOCKET NUMBER: 121 CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 303-541-3322  
TELEFAX: 303-444-3013  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10  
TYPE: amino acid  
TOPOLOGY: unknown to applicant  
MOLECULE TYPE: peptide  
HYPOTHETICAL: yes  
US-08-199-508-57

Query Match 1.5%; Score 6; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 291 SEFLHS 296  
DB 3 SEFLHS 8

RESULT 59  
US-08-912-272-46  
Sequence 46, Application US/08912272  
Patent No. 603874  
GENERAL INFORMATION:  
APPLICANT: Jofuku, K. Diane  
APPLICANT: Okamuro, Jack K.  
TITLE OF INVENTION: Methods for Improving Seeds  
NUMBER OF SEQUENCES: 103  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/912,272  
FILING DATE: 15-AUG-1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/879,827  
FILING DATE: 20-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Bastian, Kevin L.  
REGISTRATION NUMBER: 34,774  
REFERENCE/DOCKET NUMBER: 023070-067220US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-026-039-46

Query Match 1.5%; Score 6; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 STGFSR 193  
DB 5 STGFSR 10

RESULT 60  
US-09-026-039-46  
Sequence 46, Application US/09026039  
Patent No. 6329567  
GENERAL INFORMATION:  
APPLICANT: Jofuku, K. Diane  
APPLICANT: Okamuro, Jack K.  
TITLE OF INVENTION: Methods for Improving Seeds  
NUMBER OF SEQUENCES: 103  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/026,039  
FILING DATE: 19-FEB-1998  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/912,272  
FILING DATE: 15-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/879,827  
FILING DATE: 20-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Bastian, Kevin L.  
REGISTRATION NUMBER: 34,774  
REFERENCE/DOCKET NUMBER: 023070-067230US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-026-039-46

Query Match 1.5%; Score 6; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 STGFSR 193  
| | | | |  
Db 5 STGFSR 10

RESULT 61  
US-09-171-705-55  
; Sequence 55, Application US/09171705  
; Patent No. 6184204  
; GENERAL INFORMATION:  
; APPLICANT: BOOTS, ANNA M.H.  
; APPLICANT: VERHEIJDEN, GILBERTUS F.M.  
; TITLE OF INVENTION: NOVEL PEPTIDES SUITABLE FOR USE IN ANTIGEN SPECIFIC  
; TITLE OF INVENTION: IMMUNOSUPPRESSIVE THERAPY  
; FILE REFERENCE: O/96198 US  
; CURRENT APPLICATION NUMBER: US/09/171,705  
; CURRENT FILING DATE: 1999-02-09  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 55  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: DERIVED FROM  
; OTHER INFORMATION: SEQUENCE OF HUMAN CARTILAGE (HC) -39 PROTEIN  
US-09-171-705-55

Query Match 1.5%; Score 6; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 66;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 348 ALDLD 353  
| | | | |  
Db 8 ALDLD 13

RESULT 62  
US-09-171-705-56  
; Sequence 56, Application US/09171705  
; Patent No. 6184204  
; GENERAL INFORMATION:  
; APPLICANT: BOOTS, ANNA M.H.  
; APPLICANT: VERHEIJDEN, GILBERTUS F.M.  
; TITLE OF INVENTION: NOVEL PEPTIDES SUITABLE FOR USE IN ANTIGEN SPECIFIC  
; TITLE OF INVENTION: IMMUNOSUPPRESSIVE THERAPY  
; FILE REFERENCE: O/96198 US  
; CURRENT APPLICATION NUMBER: US/09/171,705  
; CURRENT FILING DATE: 1999-02-09  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 56  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: DERIVED FROM  
; OTHER INFORMATION: SEQUENCE OF HUMAN CARTILAGE (HC) -39 PROTEIN  
US-09-171-705-56

Query Match 1.5%; Score 6; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 66;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 348 ALDLD 353  
| | | | |  
Db 2 ALDLD 7

RESULT 63  
US-09-205-258-1052  
; Sequence 1052, Application US/09205258  
; Patent No. 6525174

; GENERAL INFORMATION:  
; APPLICANT: Young et al.  
; TITLE OF INVENTION: 207 Human Secreted Proteins  
; FILE REFERENCE: P2007P1  
; CURRENT APPLICATION NUMBER: US/09/205,258  
; CURRENT FILING DATE: 1998-12-04  
; EARLIER APPLICATION NUMBER: PCT/US98/11422  
; EARLIER FILING DATE: 1998-06-04  
; EARLIER APPLICATION NUMBER: 60/048,885  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/049,375  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,881  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,880  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,896  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/049,020  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,876  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,895  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,884  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,894  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,971  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,964  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,882  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,899  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,893  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,900  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,901  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,892  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,915  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/049,019  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,970  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,972  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,916  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/049,373  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,875  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/049,374  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,917  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,949  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,974  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,883  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,897  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,898  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,962

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/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,963
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,877
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,878
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/070,923
/ EARLIER FILING DATE: 1997-12-18
/ EARLIER APPLICATION NUMBER: 60/092,921
/ EARLIER FILING DATE: 1998-07-15
/ EARLIER APPLICATION NUMBER: 60/094,657
/ EARLIER FILING DATE: 1998-07-30
/ NUMBER OF SEQ ID NOS: 1227
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1052
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-205-258-1052

Query Match      1.5%; Score 6; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      333 PEASPA 338
DB      8 PEASPA 13

RESULT 64
US-09-205-258-1053
/ Sequence 1053, Application US/09205258
/ Patent No. 6525174
/ GENERAL INFORMATION:
/ APPLICANT: Young et al.
/ TITLE OF INVENTION: 207 Human Secreted Proteins
/ FILE REFERENCE: P2007P1
/ CURRENT APPLICATION NUMBER: US/09/205,258
/ CURRENT FILING DATE: 1998-12-04
/ EARLIER APPLICATION NUMBER: PCT/US98/11422
/ EARLIER FILING DATE: 1998-06-04
/ EARLIER APPLICATION NUMBER: 60/048,885
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/049,375
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,881
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,880
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,896
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/049,020
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,876
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,895
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,884
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,894
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,971
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,964
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,882
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,899
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,893
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,900

Query Match      1.5%; Score 6; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      333 PEASPA 338
DB      8 PEASPA 13

RESULT 65
PCT-US93-07653-1
/ Sequence 1, Application PC/TUS9307653
/ GENERAL INFORMATION:
/ APPLICANT: James Boyd
/ TITLE OF INVENTION: HEPARIN NEUTRALIZATION WITH
/ TITLE OF INVENTION: MUTIMERIC PEPTIDES
/ NUMBER OF SEQUENCES: 2
/ CORRESPONDENCE ADDRESS:
```

```

; ADDRESS: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07653
; FILING DATE: 19930813
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S.S.N. 07/932,456
; FILING DATE: August 17, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL T. CLARK
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00231/066WO1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18
; TYPE: amino
; STRANDEDNESS: single
; TOPOLOGY: linear
; PCT-US93-07653-1

Query Match 1.5%; Score 6; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 84 ALKKIL 89
Db 3 ALKKIL 8

RESULT 66
US-08-795-430-51
; Sequence 51, Application US/08795430
; Patent No. 6130071
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Joukov, Vladimir
; TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
; TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,430
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FI96/00427
; FILING DATE: 01-AUG-1996
; PRIOR APPLICATION DATA:

; ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/355,700
; FILING DATE: 05-No. 6361946-1999
; CLASSIFICATION: <UNKNOWN>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/795,430
; FILING DATE: 05-FEB-1997
; APPLICATION NUMBER: PCT/FI96/00427
; FILING DATE: 01-AUG-1996
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/671,573
; FILING DATE: 28-JUN-1996
; PRIOR APPLICATION DATA: 08/601,132
; APPLICATION NUMBER: 08/601,132
; FILING DATE: 14-FEB-1996
; PRIOR APPLICATION DATA: 08/585,895
; APPLICATION NUMBER: 08/585,895
; FILING DATE: 12-JAN-1996
; PRIOR APPLICATION DATA: 08/510,133
; APPLICATION NUMBER: 08/510,133
; FILING DATE: 01-AUG-1995
; PRIOR APPLICATION DATA: 08/340,011
; APPLICATION NUMBER: 08/340,011
; FILING DATE: 14-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 28967/33691
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-0448
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-795-430-51

Query Match 1.5%; Score 6; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 180 KTVSGS 185
Db 3 KTVSGS 8

RESULT 67
US-09-355-700-51
; Sequence 51, Application US/09355700
; Patent No. 6361946
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research
; APPLICANT: Helsinki University Licensing
; APPLICANT: Alitalo, Kari (U.S. only)
; APPLICANT: Joukov, Vladimir (U.S. only)
; TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
; TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/355,700
; FILING DATE: 05-No. 6361946-1999
; CLASSIFICATION: <UNKNOWN>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/795,430
; FILING DATE: 05-FEB-1997
; APPLICATION NUMBER: PCT/FI96/00427
; FILING DATE: 01-AUG-1996
; PRIOR APPLICATION DATA:

```



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; APPLICATION NUMBER: 08/671,573
; FILING DATE: 28-JUN-1996
; APPLICATION NUMBER: 08/601,132
; FILING DATE: 14-FEB-1996
; APPLICATION NUMBER: 08/585,895
; FILING DATE: 12-JAN-1996
; APPLICATION NUMBER: 08/510,133
; FILING DATE: 01-AUG-1995
; APPLICATION NUMBER: 08/340,011
; FILING DATE: 14-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 28967/34140
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-355-700-51

Query Match          1.5%; Score 6; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 180 KTVSGS 185
Db 3 KTVSGS 8

RESULT 68
5368712-4
; Patent No. 5368712
; APPLICANT: TOMICH, JOHN;MONTAL, MAURICIO
; TITLE OF INVENTION: BIOLOGICALLY MIMETIC SYNTHETIC
; ION CHANNEL TRANSDUCERS
; NUMBER OF SEQUENCES: 7
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/576,222
; FILING DATE: 31-AUG-1990
; SEQ ID NO:4:
; LENGTH: 23
5368712-4

Query Match          1.5%; Score 6; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 VFLLLT 136
Db 15 VFLLLT 20

RESULT 69
5516890-4
; Patent No. 5516890
; APPLICANT: TOMICH, JOHN;MONTAL, MAURICIO
; TITLE OF INVENTION: BIOLOGICALLY MIMETIC SYNTHETIC ION
; CHANNEL TRANSDUCERS AND METHODS OF MAKING THE SAME
; NUMBER OF SEQUENCES: 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/312,821
; FILING DATE: 27-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 576,222
; FILING DATE: 31-AUG-1990
; APPLICANT: Jofuku, K. Diane
; APPLICANT: Okamuro, Jack K.

; APPLICATION NUMBER: 430,814
; FILING DATE: 02-NOV-1989
; SEQ ID NO:4:
; LENGTH: 23
5516890-4

Query Match          1.5%; Score 6; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 VFLLLT 136
Db 15 VFLLLT 20

RESULT 70
US-08-772-440-6
; Sequence 6, Application US/08772440
; Patent No. 6046158
; GENERAL INFORMATION:
; APPLICANT: Ariizumi, Kiyoshi
; APPLICANT: Takashima, Akira
; TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
; TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/772,440
; FILING DATE: CONCURRENTLY HERewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTMD:493
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-772-440-6

Query Match          1.5%; Score 6; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 VLGAIA 19
Db 20 VLGAIA 25

RESULT 71
US-08-912-272-44
; Sequence 44, Application US/08912272
; Patent No. 6093874
; GENERAL INFORMATION:
; APPLICANT: Jofuku, K. Diane
; APPLICANT: Okamuro, Jack K.
```

;; TITLE OF INVENTION: Methods for Improving Seeds  
;; NUMBER OF SEQUENCES: 103  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Townsend and Townsend and Crew LLP  
;; STREET: Two Embarcadero Center, Eighth Floor  
;; CITY: San Francisco  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94111-3834  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/912,272  
;; FILING DATE: 15-AUG-1997  
;; CLASSIFICATION: 800  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/879,827  
;; FILING DATE: 20-JUN-1997  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/700,152  
;; FILING DATE: 20-AUG-1996  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Bastian, Kevin L.  
;; REGISTRATION NUMBER: 34,774  
;; REFERENCE/DOCKET NUMBER: 023070-067220US  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 576-0200  
;; TELEFAX: (415) 576-0300  
;; INFORMATION FOR SEQ ID NO: 44:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 26 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; FEATURE:  
;; NAME/KEY: Peptide  
;; LOCATION: 1..26  
;; OTHER INFORMATION: /note= "RAP2.7 linker region"  
;; US-08-912-272-44

Query Match 1.5%; Score 6; DB 3; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0;

QY 188 STGFSR 193  
| | | | |  
Db 20 STGFSR 25

RESULT 72  
US-09-026-039-44  
; Sequence 44, Application US/09026039  
; Patent No. 6329567  
; GENERAL INFORMATION:  
; APPLICANT: Jofuku, K. Diane  
; APPLICANT: Okamuro, Jack K.  
; TITLE OF INVENTION: Methods for Improving Seeds  
; NUMBER OF SEQUENCES: 103  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/026,039  
;; FILING DATE: 19-FEB-1998  
;; CLASSIFICATION: 800  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/912,272  
;; FILING DATE: 15-AUG-1997  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/879,827  
;; FILING DATE: 20-JUN-1997  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/700,152  
;; FILING DATE: 20-AUG-1996  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Bastian, Kevin L.  
;; REGISTRATION NUMBER: 34,774  
;; REFERENCE/DOCKET NUMBER: 023070-067230US  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 576-0200  
;; TELEFAX: (415) 576-0300  
;; INFORMATION FOR SEQ ID NO: 44:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 26 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; FEATURE:  
;; NAME/KEY: Peptide  
;; LOCATION: 1..26  
;; OTHER INFORMATION: /note= "RAP2.7 linker region"  
;; US-09-026-039-44

Query Match 1.5%; Score 6; DB 4; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0;

QY 188 STGFSR 193  
| | | | |  
Db 20 STGFSR 25

RESULT 73  
US-09-156-856-14  
; Sequence 14, Application US/09156856A  
; Patent No. 6221591  
; GENERAL INFORMATION:  
; APPLICANT: Aerts, Johannes M.  
; TITLE OF INVENTION: Determination of a genetic risk factor for infection  
; TITLE OF INVENTION: and other diseases, and detection of activated  
; TITLE OF INVENTION: phagocytes  
; FILE REFERENCE: Sequence 1-20  
; Patent No. 6221591  
; CURRENT APPLICATION NUMBER: US/09/156,856A  
; CURRENT FILING DATE: 1998-09-18  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 35  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-156-856-14

Query Match 1.5%; Score 6; DB 3; Length 35;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0;

QY 348 ALDLDD 353  
| | | | |  
Db 19 ALDLDD 24

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RESULT 74
US-09-205-258-555
; Sequence 555, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897

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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 555
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-205-258-555

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Query Match 1.5%; Score 6; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 196 QTHSSK 201
Db 9 QTHSSK 14

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RESULT 75
US-09-315-304B-1459
; Sequence 1459, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-052
; CURRENT APPLICATION NUMBER: US/09/315,304B
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1667
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1459
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-315-304B-1459

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Query Match 1.5%; Score 6; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 260 AQIQAA 265
Db 15 AQIQAA 20

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RESULT 76
US-09-515-965A-1459
; Sequence 1459, Application US/09515965A

```

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; Patent No. 6623741
; GENERAL INFORMATION:
; APPLICANT: Antczak, J.
; APPLICANT: Delmedico, M.
; APPLICANT: Erickson, J.
; APPLICANT: Lambert, D.
; APPLICANT: Sista, P.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
; FILE REFERENCE: 7872-073
; CURRENT APPLICATION NUMBER: US/09/515,965A
; CURRENT FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1994
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1459
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-515-965A-1459

Query Match          1.5%; Score 6; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 260 AQIQAA 265
Db 15 AQIQAA 20

RESULT 77
US-09-350-641C-1459
; Sequence 1459, Application US/09350641C
; Patent No. 6656906
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-067
; CURRENT APPLICATION NUMBER: US/09/350,641C
; CURRENT FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1459
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-350-641C-1459

Query Match          1.5%; Score 6; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 260 AQIQAA 265
Db 15 AQIQAA 20
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RESULT 78
US-09-124-671-5
; Sequence 5, Application US/09124671A
; Patent No. 6160088
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoo, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: 31488
; CURRENT APPLICATION NUMBER: US/09/124,671A
; CURRENT FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-124-671-5

Query Match          1.5%; Score 6; DB 3; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 LLGEVK 38
Db 17 LLGEVK 22

RESULT 79
US-08-679-493A-170
; Sequence 170, Application US/08679493A
; Patent No. 6303295
; GENERAL INFORMATION:
; APPLICANT: Taylor, Echan W.
; TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS
; FILE REFERENCE: 55-95
; CURRENT APPLICATION NUMBER: US/08/679,493A
; CURRENT FILING DATE: 1996-07-12
; PRIOR APPLICATION NUMBER: 60/001203
; PRIOR FILING DATE: 1995-07-14
; PRIOR APPLICATION NUMBER: 60/003,112
; PRIOR FILING DATE: 1995-09-01
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 170
; LENGTH: 46
; TYPE: PRT
; ORGANISM: macaque
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)..(46)
; OTHER INFORMATION: X is selenocysteine.
US-08-679-493A-170

Query Match          1.5%; Score 6; DB 4; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 222 LQELK 227
Db 14 LQELK 19

RESULT 80
US-09-205-258-399
; Sequence 399, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
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;/ CURRENT FILING DATE: 1998-12-04
;/ EARLIER APPLICATION NUMBER: PCT/US98/11422
;/ EARLIER FILING DATE: 1998-06-04
;/ EARLIER APPLICATION NUMBER: 60/048,885
;/ EARLIER FILING DATE: 1997-06-06
;/ EARLIER APPLICATION NUMBER: 60/049,375
;/ EARLIER FILING DATE: 1997-06-06
;/ EARLIER APPLICATION NUMBER: 60/048,881
;/ EARLIER FILING DATE: 1997-06-06
;/ EARLIER APPLICATION NUMBER: 60/048,880
;/ EARLIER FILING DATE: 1997-06-06
;/ EARLIER APPLICATION NUMBER: 60/048,896
;/ EARLIER FILING DATE: 1997-06-06
;/ EARLIER APPLICATION NUMBER: 60/049,020
;/ EARLIER FILING DATE: 1997-06-06
;/ EARLIER APPLICATION NUMBER: 60/048,876
;/ EARLIER FILING DATE: 1997-06-06
;/ EARLIER APPLICATION NUMBER: 60/048,895
;/ EARLIER FILING DATE: 1997-06-06
;/ EARLIER APPLICATION NUMBER: 60/048,884
;/ EARLIER FILING DATE: 1997-06-06
;/ EARLIER APPLICATION NUMBER: 60/048,894
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;/ EARLIER APPLICATION NUMBER: 60/048,871
;/ EARLIER FILING DATE: 1997-06-06
;/ EARLIER APPLICATION NUMBER: 60/048,964
;/ EARLIER FILING DATE: 1997-06-06
;/ EARLIER APPLICATION NUMBER: 60/048,882
;/ EARLIER FILING DATE: 1997-06-06
;/ EARLIER APPLICATION NUMBER: 60/048,899
;/ EARLIER FILING DATE: 1997-06-06
;/ EARLIER APPLICATION NUMBER: 60/048,893
;/ EARLIER FILING DATE: 1997-06-06
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;/ EARLIER APPLICATION NUMBER: 60/048,901
;/ EARLIER FILING DATE: 1997-06-06
;/ EARLIER APPLICATION NUMBER: 60/048,892
;/ EARLIER FILING DATE: 1997-06-06
;/ EARLIER APPLICATION NUMBER: 60/048,915
;/ EARLIER FILING DATE: 1997-06-06
;/ EARLIER APPLICATION NUMBER: 60/049,019
;/ EARLIER FILING DATE: 1997-06-06
;/ EARLIER APPLICATION NUMBER: 60/048,970
;/ EARLIER FILING DATE: 1997-06-06
;/ EARLIER APPLICATION NUMBER: 60/048,972
;/ EARLIER FILING DATE: 1997-06-06
;/ EARLIER APPLICATION NUMBER: 60/048,916
;/ EARLIER FILING DATE: 1997-06-06
;/ EARLIER APPLICATION NUMBER: 60/049,373
;/ EARLIER FILING DATE: 1997-06-06
;/ EARLIER APPLICATION NUMBER: 60/048,875
;/ EARLIER FILING DATE: 1997-06-06
;/ EARLIER APPLICATION NUMBER: 60/049,374
;/ EARLIER FILING DATE: 1997-06-06
;/ EARLIER APPLICATION NUMBER: 60/048,917
;/ EARLIER FILING DATE: 1997-06-06
;/ EARLIER APPLICATION NUMBER: 60/048,949
;/ EARLIER FILING DATE: 1997-06-06
;/ EARLIER APPLICATION NUMBER: 60/048,974
;/ EARLIER FILING DATE: 1997-06-06
;/ EARLIER APPLICATION NUMBER: 60/048,883
;/ EARLIER FILING DATE: 1997-06-06
;/ EARLIER APPLICATION NUMBER: 60/048,897
;/ EARLIER FILING DATE: 1997-06-06
;/ EARLIER APPLICATION NUMBER: 60/048,898
;/ EARLIER FILING DATE: 1997-06-06
;/ EARLIER APPLICATION NUMBER: 60/048,962
;/ EARLIER FILING DATE: 1997-06-06
;/ EARLIER APPLICATION NUMBER: 60/048,963
;/ EARLIER FILING DATE: 1997-06-06
;/ EARLIER APPLICATION NUMBER: 60/048,877
;/ EARLIER FILING DATE: 1997-06-06
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;/ EARLIER APPLICATION NUMBER: 60/048,878
;/ EARLIER FILING DATE: 1997-06-06
;/ EARLIER APPLICATION NUMBER: 60/070,923
;/ EARLIER FILING DATE: 1997-12-18
;/ EARLIER APPLICATION NUMBER: 60/092,921
;/ EARLIER FILING DATE: 1998-07-15
;/ EARLIER APPLICATION NUMBER: 60/094,657
;/ EARLIER FILING DATE: 1998-07-30
;/ NUMBER OF SEQ ID NOS: 1227
;/ SOFTWARE: Patent in Ver. 2.0
;/ SEQ ID NO 399
;/ LENGTH: 47
;/ TYPE: PRT
;/ ORGANISM: Homo sapiens
;/ FEATURE:
;/ NAME/KEY: SITE
;/ LOCATION: (47)
;/ OTHER INFORMATION: Xaa equals stop translation
US-09-205-258-399

Query Match 1.5%; Score 6; DB 4; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.8e+02; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

Qy 333 PEASPA 338
Db 40 PEASPA 45
|||||

RESULT 81
US-09-621-976-6873
; Sequence 6873, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCES: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6873
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 5
; OTHER INFORMATION: Xaa = Asp,Glu
; US-09-621-976-6873

Query Match 1.5%; Score 6; DB 4; Length 53;
Best Local Similarity 100.0%; Pred. No. 2e+02; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

Qy 336 SPASTP 341
Db 8 SPASTP 13
|||||

RESULT 82
US-09-167-681-43
; Sequence 43, Application US/09167681A
; Patent No. 6265561
; GENERAL INFORMATION:
; APPLICANT: Weinshilboum, M.D., Richard M.
; APPLICANT: Raftogiannis, Rebecca B.
; APPLICANT: Wood, Thomas C.
; APPLICANT: Ottewill, Diane M.
; TITLE OF INVENTION: SULFOTRANSFERASE SEQUENCE VARIANTS
; FILE REFERENCE: 07039/118001
```

;; CURRENT APPLICATION NUMBER: US/09/167,681A  
;; CURRENT FILING DATE: 1998-10-07  
;; NUMBER OF SEQ ID NOS: 52  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 43  
;; LENGTH: 60  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-167-681-43

Query Match 1.5%; Score 6; DB 3; Length 60;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 325 LMVHNT 330  
Db 24 LMVHNT 29

## RESULT 83

US-08-936-165A-291  
;; Sequence 291, Application US/08936165A  
;; Patent No. 6348582  
;; GENERAL INFORMATION:

;; APPLICANT: Black, Michael  
;; APPLICANT: Burnham, Martin  
;; APPLICANT: Hodgson, John  
;; APPLICANT: Knowles, David  
;; APPLICANT: Lonetto, Michael  
;; APPLICANT: Nicholas, Richard  
;; APPLICANT: Pratt, Julie  
;; APPLICANT: Reichard, Richard  
;; APPLICANT: Rosenberg, Martin  
;; APPLICANT: Ward, Judith

;; TITLE OF INVENTION: No. 6348582el Prokaryotic Polynucleotides,  
;; TITLE OF INVENTION: Polypeptides and Their Uses  
;; NUMBER OF SEQUENCES: 534  
;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: SmithKline Beecham Corporation  
;; STREET: 709 Swedeland Road  
;; CITY: King of Prussia  
;; STATE: PA  
;; COUNTRY: USA

;; ZIP: 19406-0939

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Diskette

;; COMPUTER: IBM Compatible

;; OPERATING SYSTEM: DOS

;; SOFTWARE: FastSeq for Windows Version 2.0

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/936,165A

;; FILING DATE: 24-SEP-1997

;; CLASSIFICATION: 536

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 60/027,032

;; FILING DATE: 24-SEP-1996

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Gimmi, Edward R

;; REGISTRATION NUMBER: 38,891

;; REFERENCE/DOCKET NUMBER: P50549

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 610-270-4478

;; TELEFAX: 610-270-5090

;; TELEX:

;; INFORMATION FOR SEQ ID NO: 291:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 66 amino acids

;; TYPE: amino acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; MOLECULE TYPE: Protein

US-08-936-165A-291

Query Match 1.5%; Score 6; DB 4; Length 66;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 320 VDNLT 325  
Db 47 VDNLT 52

## RESULT 84

US-09-134-000C-4727  
;; Sequence 4727, Application US/09134000C  
;; Patent No. 6617156  
;; GENERAL INFORMATION:

;; APPLICANT: Lynn Doucette-Stamm et al  
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
;; FILE REFERENCE: 032796-032  
;; CURRENT APPLICATION NUMBER: US/09/134,000C  
;; CURRENT FILING DATE: 1998-08-13  
;; PRIOR APPLICATION NUMBER: US 60/055,778  
;; PRIOR FILING DATE: 1997-08-15  
;; NUMBER OF SEQ ID NOS: 6812  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 4727  
;; LENGTH: 66  
;; TYPE: PRT  
;; ORGANISM: Enterococcus faecalis  
US-09-134-000C-4727

Query Match 1.5%; Score 6; DB 4; Length 66;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 VVANLG 172  
Db 43 VVANLG 48

## RESULT 85

US-09-716-129-52  
;; Sequence 52, Application US/09716129  
;; Patent No. 6632920  
;; GENERAL INFORMATION:

;; APPLICANT: Rosen et al.  
;; TITLE OF INVENTION: 36 Human Secreted Proteins  
;; FILE REFERENCE: P2025P1  
;; CURRENT APPLICATION NUMBER: US/09/716,129  
;; CURRENT FILING DATE: 2000-11-17  
;; PRIOR APPLICATION NUMBER: 60/076,053  
;; PRIOR FILING DATE: 1998-02-26  
;; PRIOR APPLICATION NUMBER: 60/076,057  
;; PRIOR FILING DATE: 1998-02-26  
;; PRIOR APPLICATION NUMBER: 60/076,052  
;; PRIOR FILING DATE: 1998-02-26  
;; PRIOR APPLICATION NUMBER: 60/076,054  
;; PRIOR FILING DATE: 1998-02-26  
;; PRIOR APPLICATION NUMBER: 60/076,051  
;; PRIOR FILING DATE: 1998-02-26  
;; NUMBER OF SEQ ID NOS: 186  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 52  
;; LENGTH: 66  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; FEATURE:

;; NAME/KEY: SITE

;; LOCATION: (66)

;; OTHER INFORMATION: Xaa equals stop translation

US-09-716-129-52

Query Match 1.5%; Score 6; DB 4; Length 66;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;

[illegible]

RESULT 87  
US-09-308-003-15  
; Sequence 15, Application US/09308003  
; Patent No. 6326170  
; GENERAL INFORMATION:  
; APPLICANT: Burnham, Martin K. R.  
; APPLICANT: Lonetto, Michael A.  
; APPLICANT: Warren, Patrick V.  
; TITLE OF INVENTION: NOVEL PROKARYOTIC POLYNUCLEOTIDES,  
; FILE REFERENCE: GMI0093  
; CURRENT APPLICATION NUMBER: US/09/308,003  
; CURRENT FILING DATE: 1999-05-10  
; EARLIER APPLICATION NUMBER: 60/058,710  
; EARLIER FILING DATE: 1997-09-12  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 15  
; LENGTH: 69  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
US-09-308-003-15  
  
Query Match 1.5%; Score 6; DB 4; Length 69;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 320 VDNLT 325  
DB 50 VDNLT 55  
|||||  
  
RESULT 88  
US-08-280-443-25  
; Sequence 25, Application US/08280443  
; Patent No. 5643778  
; GENERAL INFORMATION:  
; APPLICANT: Nishikura, Kazuko  
; TITLE OF INVENTION: RNA Editing Enzyme and Methods of Use  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Howson and Howson  
; STREET: Spring House Corporate Cntr, P.O. Box 457  
; CITY: Spring House  
; STATE: Pennsylvania  
; COUNTRY: USA  
; ZIP: 19477  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/280,443  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/197,794  
; FILING DATE: 17-FEB-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bak, Mary E.  
; REGISTRATION NUMBER: 31,215  
; REFERENCE/DOCKET NUMBER: WST49AUSA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-540-9206  
; TELEFAX: 215-540-5818  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 73 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein

EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,892  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/057,761  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/047,595  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,599  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,588  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,585  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,586  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,590  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,594  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,589  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,593  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,614  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/043,578  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,576  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/047,501  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/043,670  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/056,632  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,664  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,876  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,862  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,887  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,909  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,875  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,862  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,887  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,908  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/048,964  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/057,650  
; EARLIER FILING DATE: 1997-09-05  
; EARLIER APPLICATION NUMBER: 60/056,884  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/057,669  
; EARLIER FILING DATE: 1997-09-05  
; EARLIER APPLICATION NUMBER: 60/049,610  
; EARLIER FILING DATE: 1997-06-13  
; EARLIER APPLICATION NUMBER: 60/061,060  
; EARLIER FILING DATE: 1997-10-02  
  
Query Match 1.5%; Score 6; DB 4; Length 67;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 367 DKRSKA 372  
DB 42 DKRSKA 47  
|||||



US-08-280-443-25

Query Match 1.5%; Score 6; DB 1; Length 73;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 82 EQALKK 87  
| | | | |  
Db 64 EQALKK 69

RESULT 89

US-08-457-459-25  
; Sequence 25, Application US/08457459  
; Patent No. 5677428  
; GENERAL INFORMATION:  
; APPLICANT: Nishikura, Kazuko  
; TITLE OF INVENTION: RNA Editing Enzyme and Methods of Use  
; TITLE OF INVENTION: Thereof  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Howson and Howson  
; STREET: Spring House Corporate Cntr, P.O. Box 457  
; CITY: Spring House  
; STATE: Pennsylvania  
; COUNTRY: USA  
; ZIP: 19477  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/457,459  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/197,794  
; FILING DATE: 17-FEB-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/280,443  
; FILING DATE: 25-JUL-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bak, Mary E.  
; REGISTRATION NUMBER: 31,215  
; REFERENCE/DOCKET NUMBER: WST49CUSA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-540-9206  
; TELEFAX: 215-540-5818  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 73 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
US-08-457-459-25

Query Match 1.5%; Score 6; DB 1; Length 73;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 82 EQALKK 87  
| | | | |  
Db 64 EQALKK 69

RESULT 90

US-08-555-678-25  
; Sequence 25, Application US/08555678  
; Patent No. 5763174  
; GENERAL INFORMATION:  
; APPLICANT: Nishikura, Kazuko  
; TITLE OF INVENTION: RNA Editing Enzyme and Methods

; TITLE OF INVENTION: of Use Thereof  
; NUMBER OF SEQUENCES: 67  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Howson and Howson  
; STREET: Spring House Corporate Cntr, P.O. Box 457  
; CITY: Spring House  
; STATE: Pennsylvania  
; COUNTRY: USA  
; ZIP: 19477  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/555,678  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/197,794  
; FILING DATE: 17-FEB-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/280,443  
; FILING DATE: 25-JUL-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/457,459  
; FILING DATE: 01-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bak, Mary E.  
; REGISTRATION NUMBER: 31,215  
; REFERENCE/DOCKET NUMBER: WST49DUSA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-540-9206  
; TELEFAX: 215-540-5818  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 73 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
US-08-555-678-25

Query Match 1.5%; Score 6; DB 1; Length 73;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 82 EQALKK 87  
| | | | |  
Db 64 EQALKK 69

RESULT 91

PCT-US95-02275-25  
; Sequence 25, Application PC/TUS9502275  
; GENERAL INFORMATION:  
; APPLICANT: Wistar Institute of Anatomy & Biology  
; TITLE OF INVENTION: RNA Editing Enzyme and Methods of Use  
; TITLE OF INVENTION: Thereof  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Howson and Howson  
; STREET: Spring House Corporate Cntr, P.O. Box 457  
; CITY: Spring House  
; STATE: Pennsylvania  
; COUNTRY: USA  
; ZIP: 19477  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:

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/ APPLICATION NUMBER: PCT/US95/02275
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION NUMBER: US 08/280,443
/ APPLICATION NUMBER: US 08/280,443
/ FILING DATE: 25-JUL-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/197,794
/ FILING DATE: 17-FEB-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bak, Mary E.
/ REGISTRATION NUMBER: 31,215
/ REFERENCE/DOCKET NUMBER: WST49BPCT
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 215-540-9206
/ TELEFAX: 215-540-5818
/ INFORMATION FOR SEQ ID NO: 25:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 73 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
PCT-US95-02275-25

Query Match 1.5%; Score 6; DB 5; Length 73;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 EQALKK 87
Db 64 EQALKK 69

RESULT 92
US-09-621-976-6090
/ Sequence 6090, Application US/09621976
/ Patent No. 6639063
/ GENERAL INFORMATION:
/ APPLICANT: Dumas Milne Edwards, J.B.
/ APPLICANT: Jobert, S.
/ APPLICANT: Giordano, J.Y.
/ TITLE OF INVENTION: ESTs and Encoded Human Proteins.
/ FILE REFERENCE: GENSET.054PR2
/ CURRENT APPLICATION NUMBER: US/09/621,976
/ CURRENT FILING DATE: 2000-07-21
/ NUMBER OF SEQ ID NOS: 19335
/ SOFTWARE: Patent.pm
/ SEQ ID NO 6090
/ LENGTH: 74
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-621-976-6090

Query Match 1.5%; Score 6; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 LVFLLL 135
Db 64 LVFLLL 69

RESULT 93
US-09-489-039A-13015
/ Sequence 13015, Application US/09489039A
/ Patent No. 6610836
/ GENERAL INFORMATION:
/ APPLICANT: Gary Breton et. al
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
/ TITLE OF INVENTION: PNEUMONIA FOR DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: 2709.2004001
/ CURRENT APPLICATION NUMBER: US/09/489,039A

/ APPLICATION NUMBER: US 60/117,747
/ PRIOR FILING DATE: 1999-01-29
/ NUMBER OF SEQ ID NOS: 14342
/ SEQ ID NO 13015
/ LENGTH: 75
/ TYPE: PRT
/ ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13015

Query Match 1.5%; Score 6; DB 4; Length 75;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 LVFLLL 135
Db 57 LVFLLL 62

RESULT 94
US-07-881-075-16
/ Sequence 16, Application US/07881075
/ Patent No. 5444149
/ GENERAL INFORMATION:
/ APPLICANT: KEENE, JACK D.
/ APPLICANT: KING, PETER H.
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL IN THE
/ TITLE OF INVENTION: RECOGNITION, BINDING AND EXPRESSION OF RIBONUCLEIC ACIDS
/ TITLE OF INVENTION: INVOLVED IN CELL GROWTH, NEOPLASIA AND IMMUNOREGULATION
/ NUMBER OF SEQUENCES: 51
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
/ ADDRESSEE: P.C.
/ STREET: 1755 Jefferson Davis Highway, Fourth Floor
/ CITY: Arlington
/ STATE: Virginia
/ COUNTRY: U.S.A.
/ ZIP: 22202
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/881,075
/ FILING DATE: 19920511
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Oblon, No. 5444149man F.
/ REGISTRATION NUMBER: 24,618
/ REFERENCE/DOCKET NUMBER: 714-154-0
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703)521-4500
/ TELEFAX: (703)486-2347
/ TELEX: 248855 OPAT UR
/ INFORMATION FOR SEQ ID NO: 16:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 80 amino acids
/ TYPE: AMINO ACID
/ TOPOLOGY: unknown
/ MOLECULE TYPE: peptide
US-07-881-075-16

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Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 223 QEELKS 228
Db 13 QEELKS 18
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RESULT 95
US-08-120-827-16
; Sequence 16, Application US/08120827
; Patent No. 5525495
; GENERAL INFORMATION:
; APPLICANT: KEENE, JACK D.
; APPLICANT: KING, PETER H.
; APPLICANT: LEVINE, TODD
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL IN THE
; TITLE OF INVENTION: RECOGNITION, BINDING AND EXPRESSION OF RIBONUCLEIC ACIDS
; TITLE OF INVENTION: INVOLVED IN CELL GROWTH, NEOPLASIA AND IMMUNOREGULATION
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/120,827
; FILING DATE: 15-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5525495man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 714-158-0 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)413-3000
; TELEFAX: (703)413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-120-827-16

Query Match 1.5%; Score 6; DB 1; Length 80;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 223 QEELKS 228
Db 13 QEELKS 18

RESULT 96
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; Sequence 16, Application US/08478675
; Patent No. 5773246
; GENERAL INFORMATION:
; APPLICANT: KEENE, JACK D.
; APPLICANT: KING, PETER H.
; APPLICANT: LEVINE, TODD
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL IN THE
; TITLE OF INVENTION: RECOGNITION, BINDING AND EXPRESSION OF RIBONUCLEIC ACIDS
; TITLE OF INVENTION: INVOLVED IN CELL GROWTH, NEOPLASIA AND IMMUNOREGULATION
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.

Query Match 1.5%; Score 6; DB 1; Length 80;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 223 QEELKS 228
Db 13 QEELKS 18

RESULT 97
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; Sequence 3983, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 3983
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -24...-1
US-09-621-976-3983

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Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 LLLTPS 138
Db 53 LLLTPS 58

RESULT 98
US-08-851-843A-220
; Sequence 220, Application US/08851843A
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; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-00293005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 220:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 91 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-851-843A-220

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Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 336 SPASTP 341
Db 44 SPASTP 49
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; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-00261005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 339:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 91 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-974-549A-339

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Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 336 SPASTP 341
Db 44 SPASTP 49
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; Sequence 339, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
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Db 44 SPASTP 49

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US-08-854-050-220  
; Sequence 220, Application US/08854050  
; Patent No. 6261836  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Harley, Calvin  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: No. 6261836el Telomerase  
; NUMBER OF SEQUENCES: 225  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/854,050  
; FILING DATE: 09-MAY-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002930US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 220:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 91 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-854-050-220

Query Match 1.5%; Score 6; DB 3; Length 91;  
Best Local Similarity 100.0%; Pred. No. 3.2e-02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 336 SPASTP 341  
Db 44 SPASTP 49

GenCore version 5.1.6  
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Minimum DB seq length: 0

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Post-processing: Listing first 500 summaries

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- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
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- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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136	409	100.0	409	6	ABR69724	Human	sec	209	409	100.0	409	6	ABR90621	Human	sec
137	409	100.0	409	6	ABU80101	Human	PRO	210	409	100.0	409	6	ABR73689	Human	sec
138	409	100.0	409	6	ABU82485	Novel	hum	211	409	100.0	409	6	ABO16941	Human	sec
139	409	100.0	409	6	ABU92144	Novel	hum	212	409	100.0	409	6	ABR94366	Human	sec
140	409	100.0	409	6	ABU93370	Human	PRO	213	409	100.0	409	6	ABR75873	Human	sec
141	409	100.0	409	6	ABO03923	Human	sec	214	409	100.0	409	6	ABR71249	Human	sec
142	409	100.0	409	6	ABO09008	Human	sec	215	409	100.0	409	6	ABR93146	Human	sec
143	409	100.0	409	6	ABU96449	Human	PRO	216	409	100.0	409	6	ABR93451	Human	sec
144	409	100.0	409	6	ABU10850	Human	PRO	217	409	100.0	409	6	ADA10142	Human	sec
145	409	100.0	409	6	ABU10576	Human	sec	218	409	100.0	409	6	ABR87876	Human	sec
146	409	100.0	409	6	ABU81602	Novel	hum	219	409	100.0	409	6	ABO27876	Human	sec
147	409	100.0	409	6	ABU72119	Human	PRO	220	409	100.0	409	6	ABO30011	Human	sec
148	409	100.0	409	6	ABU95585	Human	PRO	221	409	100.0	409	6	ABO33220	Human	PRO
149	409	100.0	409	6	ABU96794	Novel	hum	222	409	100.0	409	6	ABM04908	Human	sec
150	409	100.0	409	6	ABR70639	Human	sec	223	409	100.0	409	6	ABM08868	Human	sec
151	409	100.0	409	6	ABO04990	Novel	hum	224	409	100.0	409	6	ABO36468	Human	sec
152	409	100.0	409	6	ABO08398	Human	sec	225	409	100.0	409	6	ABO36553	Human	PRO
153	409	100.0	409	6	ABR89541	Human	sec	226	409	100.0	409	6	ABO39518	Human	sec
154	409	100.0	409	6	ABO34055	Human	PRO	227	409	100.0	409	6	ABM10393	Human	sec
155	409	100.0	409	6	ABO05605	Human	sec	228	409	100.0	409	6	ABM11918	Human	sec
156	409	100.0	409	6	ABR73994	Human	sec	229	409	100.0	409	6	ABO52064	Human	PRO
157	409	100.0	409	6	ABR95586	Human	sec	230	409	100.0	409	6	ABO52369	Human	PRO
158	409	100.0	409	6	ABR80883	Human	sec	231	409	100.0	409	6	ADA19884	Novel	hum
159	409	100.0	409	6	ABR81188	Human	sec	232	409	100.0	409	6	ABO23687	Human	sec
160	409	100.0	409	6	ABM00884	Human	sec	233	409	100.0	409	6	ABD17267	Human	tra
161	409	100.0	409	6	ABR8486	Human	sec	234	409	100.0	409	6	ADA17686	Human	PRO
162	409	100.0	409	6	ABM77307	Human	sec	235	409	100.0	409	6	ABR97173	Human	sec
163	409	100.0	409	6	ABO28791	Human	sec	236	409	100.0	409	6	ABR86961	Human	sec
164	409	100.0	409	6	ABO31536	Human	sec	237	409	100.0	409	6	ABM11003	Human	sec
165	409	100.0	409	6	ABM07953	Human	sec	238	409	100.0	409	6	ABM28147	Human	sec
166	409	100.0	409	6	ABO40433	Human	sec	239	409	100.0	409	6	ABO32146	Human	sec
167	409	100.0	409	6	ABO35858	Human	PRO	240	409	100.0	409	6	ABM15273	Human	sec
168	409	100.0	409	6	ABO43997	Human	PRO	241	409	100.0	409	6	ABM06428	Human	sec
169	409	100.0	409	6	ADA77886	Human	sec	242	409	100.0	409	6	ABM04239	Human	sec
170	409	100.0	409	6	ABM24792	Human	sec	243	409	100.0	409	6	ABM22352	Human	sec
171	409	100.0	409	6	ABO03060	Human	sec	244	409	100.0	409	6	ABM07648	Human	sec







PR 04-JUN-1998;	98US-0088326P.	PR 02-JUL-1998;	98US-0091633P.
PR 05-JUN-1998;	98US-0088167P.	PR 02-JUL-1998;	98US-0091646P.
PR 05-JUN-1998;	98US-0088202P.	PR 02-JUL-1998;	98US-0091673P.
PR 05-JUN-1998;	98US-0088212P.	PR 07-JUL-1998;	98US-0091978P.
PR 05-JUN-1998;	98US-0088217P.	PR 07-JUL-1998;	98US-0091982P.
PR 09-JUN-1998;	98US-0088655P.	PR 09-JUL-1998;	98US-0092182P.
PR 10-JUN-1998;	98US-0088722P.	PR 10-JUL-1998;	98US-0092472P.
PR 10-JUN-1998;	98US-0088730P.	PR 20-JUL-1998;	98US-0093339P.
PR 10-JUN-1998;	98US-0088734P.	PR 30-JUL-1998;	98US-0094651P.
PR 10-JUN-1998;	98US-0088738P.	PR 04-AUG-1998;	98US-0095282P.
PR 10-JUN-1998;	98US-0088740P.	PR 04-AUG-1998;	98US-0095285P.
PR 10-JUN-1998;	98US-0088741P.	PR 04-AUG-1998;	98US-0095301P.
PR 10-JUN-1998;	98US-0088742P.	PR 04-AUG-1998;	98US-0095302P.
PR 10-JUN-1998;	98US-0088810P.	PR 04-AUG-1998;	98US-0095318P.
PR 10-JUN-1998;	98US-0088811P.	PR 04-AUG-1998;	98US-0095321P.
PR 10-JUN-1998;	98US-0088824P.	PR 04-AUG-1998;	98US-0095325P.
PR 10-JUN-1998;	98US-0088825P.	PR 10-AUG-1998;	98US-0095316P.
PR 10-JUN-1998;	98US-0088826P.	PR 10-AUG-1998;	98US-0095329P.
PR 11-JUN-1998;	98US-0088858P.	PR 10-AUG-1998;	98US-0096012P.
PR 11-JUN-1998;	98US-0088861P.	PR 10-AUG-1998;	98US-0096012P.
PR 11-JUN-1998;	98US-0088863P.	PR 11-AUG-1998;	98US-0096143P.
PR 11-JUN-1998;	98US-0088866P.	PR 11-AUG-1998;	98US-0096146P.
PR 11-JUN-1998;	98US-0088876P.	PR 12-AUG-1998;	98US-0096329P.
PR 12-JUN-1998;	98US-0089090P.	PR 17-AUG-1998;	98US-0096757P.
PR 12-JUN-1998;	98US-0089105P.	PR 17-AUG-1998;	98US-0096766P.
PR 16-JUN-1998;	98US-0089440P.	PR 17-AUG-1998;	98US-0096768P.
PR 16-JUN-1998;	98US-0089512P.	PR 17-AUG-1998;	98US-0096773P.
PR 16-JUN-1998;	98US-0089514P.	PR 17-AUG-1998;	98US-0096791P.
PR 17-JUN-1998;	98US-0089532P.	PR 17-AUG-1998;	98US-0096867P.
PR 17-JUN-1998;	98US-0089538P.	PR 17-AUG-1998;	98US-0096891P.
PR 17-JUN-1998;	98US-0089598P.	PR 17-AUG-1998;	98US-0096894P.
PR 17-JUN-1998;	98US-0089599P.	PR 17-AUG-1998;	98US-0096895P.
PR 17-JUN-1998;	98US-0089600P.	PR 17-AUG-1998;	98US-0096897P.
PR 17-JUN-1998;	98US-0089653P.	PR 18-AUG-1998;	98US-0096949P.
PR 18-JUN-1998;	98US-0089801P.	PR 18-AUG-1998;	98US-0096950P.
PR 18-JUN-1998;	98US-0089907P.	PR 18-AUG-1998;	98US-0096956P.
PR 18-JUN-1998;	98US-0089908P.	PR 18-AUG-1998;	98US-0097022P.
PR 19-JUN-1998;	98US-0089947P.	PR 19-AUG-1998;	98US-0097141P.
PR 19-JUN-1998;	98US-0089948P.	PR 20-AUG-1998;	98US-0097218P.
PR 19-JUN-1998;	98US-0089952P.	PR 24-AUG-1998;	98US-0097861P.
PR 22-JUN-1998;	98US-0090246P.	PR 24-AUG-1998;	98US-0097951P.
PR 22-JUN-1998;	98US-0090252P.	PR 26-AUG-1998;	98US-0097952P.
PR 22-JUN-1998;	98US-0090254P.	PR 26-AUG-1998;	98US-0097952P.
PR 23-JUN-1998;	98US-0090349P.	PR 26-AUG-1998;	98US-0097954P.
PR 23-JUN-1998;	98US-0090355P.	PR 26-AUG-1998;	98US-0097955P.
PR 24-JUN-1998;	98US-0090429P.	PR 26-AUG-1998;	98US-0097971P.
PR 24-JUN-1998;	98US-0090431P.	PR 26-AUG-1998;	98US-0097974P.
PR 24-JUN-1998;	98US-0090433P.	PR 26-AUG-1998;	98US-0097978P.
PR 24-JUN-1998;	98US-0090444P.	PR 26-AUG-1998;	98US-0097979P.
PR 24-JUN-1998;	98US-0090445P.	PR 26-AUG-1998;	98US-0097986P.
PR 24-JUN-1998;	98US-0090461P.	PR 26-AUG-1998;	98US-0098014P.
PR 24-JUN-1998;	98US-0090472P.	PR 31-AUG-1998;	98US-0098525P.
PR 24-JUN-1998;	98US-0090535P.	PR 16-SEP-1998;	98US-0100634P.
PR 24-JUN-1998;	98US-0090538P.	PR 12-JAN-1999;	99US-0115565P.
PR 24-JUN-1998;	98US-0090540P.	XX (GETH ) GENENTECH INC.	
PR 24-JUN-1998;	98US-0090557P.	PA Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;	
PR 25-JUN-1998;	98US-0090676P.	PI Wood WI, Yuan J;	
PR 25-JUN-1998;	98US-0090678P.	PI WPI; 2000-072883/06.	
PR 25-JUN-1998;	98US-0090688P.	XX N-PSDB; AAZ64999.	
PR 25-JUN-1998;	98US-0090690P.	XX Membrane-bound proteins and related nucleotide sequences.	
PR 25-JUN-1998;	98US-0090693P.	XX Claim 12; Fig 95; 822pp; English.	
PR 25-JUN-1998;	98US-0090694P.	XX The invention provides membrane-bound PRO polypeptides and	
PR 25-JUN-1998;	98US-0090695P.	XX polynucleotides encoding them. The PRO sequences of the invention were	
PR 25-JUN-1998;	98US-0090696P.	XX identified based on extracellular domain homology screening. The PRO	
PR 26-JUN-1998;	98US-0090862P.	XX sequences have homology with proteins including LDL receptors, TIE	
PR 01-JUL-1998;	98US-0091358P.	XX ligands and various enzymes. The membrane-bound proteins and receptor	
PR 02-JUL-1998;	98US-0091360P.	XX molecules are useful as pharmaceutical and diagnostic agents. Receptor	
PR 02-JUL-1998;	98US-0091478P.	XX immunoadhesins, for instance, can be used as therapeutic agents to block	
PR 02-JUL-1998;	98US-0091486P.		
PR 02-JUL-1998;	98US-0091519P.		
PR 02-JUL-1998;	98US-0091544P.		
PR 02-JUL-1998;	98US-0091626P.		
PR 02-JUL-1998;	98US-0091628P.		

CC receptor-ligand interactions. The membrane-bound proteins can also be  
CC employed for screening of potential peptide or small molecule inhibitors  
CC of the relevant receptor/ligand interaction. The PRO encoding sequences  
CC are useful as hybridization probes, in chromosome and gene mapping and in  
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will  
CC also be useful for the preparation of PRO polypeptides, especially by  
CC recombinant techniques  
XX  
SQ Sequence 409 AA;

Query Match 100.0%; Score 409; DB 3; Length 409;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGESTSAVLGSGFVLGALAFQHLNLTSDTEGFLGVEKGEAKNSITDSQMDVVEVYITD 60  
DB 1 MEGESTSAVLGSGFVLGALAFQHLNLTSDTEGFLGVEKGEAKNSITDSQMDVVEVYITD 60  
QY 61 IQYIIPCQLPSFYNSGGEVNEQALKKILSNVKNVGVWYKFRHSDQIMTFRRLHKN 120  
DB 61 IQYIIPCQLPSFYNSGGEVNEQALKKILSNVKNVGVWYKFRHSDQIMTFRRLHKN 120  
QY 121 LQEHFSNODLVLLLTPTSIITSCSTHRLHSLYKPKQGLFHRVPLVAVANLGMSEQLGYK 180  
DB 121 LQEHFSNODLVLLLTPTSIITSCSTHRLHSLYKPKQGLFHRVPLVAVANLGMSEQLGYK 180  
QY 181 TVSGSCMTGFRVAVOTHSSKFFEDGSLKEVHKINEMVYASLOELKSI CKKVEDSEAV 240  
DB 181 TVSGSCMTGFRVAVOTHSSKFFEDGSLKEVHKINEMVYASLOELKSI CKKVEDSEAV 240  
QY 241 DKLVKDVNLRKREIEKRGQAQQAAREKNIQKDPENIFLCOALRFFPNSEFLHSCVMS 300  
DB 241 DKLVKDVNLRKREIEKRGQAQQAAREKNIQKDPENIFLCOALRFFPNSEFLHSCVMS 300  
QY 301 LKNRHSKSSCNVNHLDVVDNLTLVHTDIPEASPASTPQIIKHKALDLDNRWQFKRS 360  
DB 301 LKNRHSKSSCNVNHLDVVDNLTLVHTDIPEASPASTPQIIKHKALDLDNRWQFKRS 360  
QY 361 RLIDTQDKRSKANTGSSNQDKASKSSPETDEIEKMGKGFYSRSPF 409  
DB 361 RLIDTQDKRSKANTGSSNQDKASKSSPETDEIEKMGKGFYSRSPF 409

# RESULT 2

ID AAU29090 standard; protein; 409 AA.  
XX  
AC AAU29090;  
XX  
DT 18-DEC-2001 (first entry)  
XX  
DE Human PRO polypeptide sequence #67.  
XX  
KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;  
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;  
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;  
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200168848-A2.  
XX  
PD 20-SEP-2001.  
XX  
PF 28-FEB-2001; 2001WO-US006520.  
XX  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 03-MAR-2000; 2000US-0187202P.  
PR 06-MAR-2000; 2000US-0186968P.  
PR 14-MAR-2000; 2000US-0189320P.  
PR 15-MAR-2000; 2000US-0189328P.  
PR 15-MAR-2000; 2000WO-US006884.

PR 21-MAR-2000; 2000US-0190828P.  
PR 21-MAR-2000; 2000US-0191007P.  
PR 21-MAR-2000; 2000US-0191048P.  
PR 21-MAR-2000; 2000US-0191314P.  
PR 28-MAR-2000; 2000US-0192655P.  
PR 28-MAR-2000; 2000US-0193032P.  
PR 28-MAR-2000; 2000US-0193053P.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 04-APR-2000; 2000US-0194449P.  
PR 04-APR-2000; 2000US-0194647P.  
PR 11-APR-2000; 2000US-0195975P.  
PR 11-APR-2000; 2000US-0196000P.  
PR 11-APR-2000; 2000US-0196187P.  
PR 11-APR-2000; 2000US-0196690P.  
PR 11-APR-2000; 2000US-0196820P.  
PR 18-APR-2000; 2000US-0198121P.  
PR 18-APR-2000; 2000US-0198585P.  
PR 25-APR-2000; 2000US-0199397P.  
PR 25-APR-2000; 2000US-0199550P.  
PR 25-APR-2000; 2000US-0199654P.  
PR 03-MAY-2000; 2000US-0201516P.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 05-JUN-2000; 2000US-0209832P.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 22-AUG-2000; 2000US-00644848.  
PR 22-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000WO-US034956.

(GETH ) GENENTECH INC.

Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;  
Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

WPI; 2001-602746/68.  
N-PSDB; AAS45991.

Novel nucleic acids encoding PRO polypeptides, used to diagnose the  
presence of tumors, such as prostate and breast tumors, in mammals and to  
screen for modulators of the compounds.

Claim 11; Fig 134; 774pp; English.

Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.  
The PRO polypeptides and their associated nucleic acids can be used to  
detect the presence of a tumour in a mammal by comparing the level of  
expression of a PRO polypeptide in a test sample of cells from the animal  
and a control sample of normal cells, whereby a higher level of  
expression in the test sample indicates the presence of a tumour in the  
mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats  
and rabbits but are preferably human. The polypeptides can be used to  
stimulate tumour necrosis factor (TNF) alpha release from human blood,  
when contacted with it. A specific polypeptide can be used to stimulate  
the proliferation or differentiation of chondrocyte cells. The PRO  
proteins can be used to determine the presence of tumours and also  
susceptibility to tumour development, particularly adrenal, lung, colon,  
breast, prostate, rectal, cervical, or liver tumours, in mammalian  
subjects. The oligonucleotide probes specific for the PRO nucleic acids  
can be used for genetic analysis of individuals with genetic disorders

Sequence 409 AA;

Query Match 100.0%; Score 409; DB 4; Length 409;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGESTSAVLGSGFVLGALAFQHLNLTSDTEGFLGVEKGEAKNSITDSQMDVVEVYITD 60  
DB 1 MEGESTSAVLGSGFVLGALAFQHLNLTSDTEGFLGVEKGEAKNSITDSQMDVVEVYITD 60

QY 61 IQKIYPCYQLFSFYNSGVEVNEQALKKILSNVKNVGVYKFRHSDQIMTFRRLLHKN 120  
PS 61 IQKIYPCYQLFSFYNSGVEVNEQALKKILSNVKNVGVYKFRHSDQIMTFRRLLHKN 120  
CC 121 LQEHFSDQDLVFLLLTPSIITSCSTHRLHSLYKPKGLFHRVPLVAVANLGMSEQLGYK 180  
CC 121 LQEHFSDQDLVFLLLTPSIITSCSTHRLHSLYKPKGLFHRVPLVAVANLGMSEQLGYK 180  
CC 121 LQEHFSDQDLVFLLLTPSIITSCSTHRLHSLYKPKGLFHRVPLVAVANLGMSEQLGYK 180  
CC 121 LQEHFSDQDLVFLLLTPSIITSCSTHRLHSLYKPKGLFHRVPLVAVANLGMSEQLGYK 180  
QY 181 TVSGSCMTGFSRAVQTHSSKFFEDGSLKEVHKINEMYASIQBELKSIKKVEDSEQAV 240  
PS 181 TVSGSCMTGFSRAVQTHSSKFFEDGSLKEVHKINEMYASIQBELKSIKKVEDSEQAV 240  
QY 241 DKLVKDVNRLKREIEKRRGAQIQAAAREKNIQKDPQENIFLCOALRTFFPNSFHLSCVMS 300  
PS 241 DKLVKDVNRLKREIEKRRGAQIQAAAREKNIQKDPQENIFLCOALRTFFPNSFHLSCVMS 300  
QY 301 LKQNRHVSKSSCNYNHLDVVDNLTLMVHTDIPEASPASTPQIIKHKALDLDLDRWQFKRS 360  
PS 301 LKQNRHVSKSSCNYNHLDVVDNLTLMVHTDIPEASPASTPQIIKHKALDLDLDRWQFKRS 360  
QY 361 RLDDTQDKRSKANTGSSNQDKASKMSPETDEIEKMGFGFYSRSPTF 409  
PS 361 RLDDTQDKRSKANTGSSNQDKASKMSPETDEIEKMGFGFYSRSPTF 409  
RESULT 3  
ID AAB87536 standard; protein; 409 AA.  
AC AAB87536;  
DT 15-MAY-2001 (first entry)  
XX Human PRO1013.  
XX Human; PRO protein; mapping.  
XX Homo sapiens.  
XX WO200116318-A2.  
XX 08-MAR-2001.  
XX 24-AUG-2000; 2000WO-US023328.  
XX 01-SEP-1999; 99WO-US020111.  
XX 15-SEP-1999; 99WO-US021090.  
XX 07-DEC-1999; 99US-0169493P.  
XX 09-DEC-1999; 99US-0170262P.  
XX 11-JAN-2000; 2000US-0175481P.  
XX 18-FEB-2000; 2000WO-US004341.  
XX 18-FEB-2000; 2000WO-US004342.  
XX 22-FEB-2000; 2000WO-US004414.  
XX 01-MAR-2000; 2000WO-US005601.  
XX 03-MAR-2000; 2000US-0187202P.  
XX 21-MAR-2000; 2000US-0191007P.  
XX 30-MAR-2000; 2000WO-US008439.  
XX 25-APR-2000; 2000US-0199397P.  
XX 22-MAY-2000; 2000WO-US014042.  
XX 05-JUN-2000; 2000US-0209832P.  
XX (GETH ) GENENTECH INC.  
XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;  
XX DR N-PSDB; AA92068.  
XX WPI: 2001-183260/18.  
XX N-PSDB; AA92068.  
XX Eighty four nucleic acids encoding PRO polypeptides, useful in molecular  
PT biology, including use as hybridization probes, and in chromosome and  
PT gene mapping.

XX Claim 12; Fig 22; 278pp; English.  
XX The present sequence is a human PRO polypeptide (secreted and  
CC transmembrane) The PRO protein, and PRO agonists, PRO antagonists or  
CC anti-PRO antibodies are useful for preparation of a medicament useful in  
CC the treatment of a condition which is responsive to the PRO protein,  
CC agonists, antagonists or anti-PRO antibodies. The PRO protein may also be  
CC employed as molecular weight markers for protein electrophoresis. The PRO  
CC coding sequence has applications in molecular biology, including use as  
CC hybridisation probes, and in chromosome and gene mapping  
XX Sequence 409 AA;  
SQ Query Match 100.0%; Score 409; DB 4; Length 409;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MEGESTSAVLGSLGALAFQHLNTDSDTEGFLGKGEAKNSITDSQMDVVEVYITD 60  
DB 1 MEGESTSAVLGSLGALAFQHLNTDSDTEGFLGKGEAKNSITDSQMDVVEVYITD 60  
QY 61 IQKIYPCYQLFSFYNSGVEVNEQALKKILSNVKNVGVYKFRHSDQIMTFRRLLHKN 120  
DB 61 IQKIYPCYQLFSFYNSGVEVNEQALKKILSNVKNVGVYKFRHSDQIMTFRRLLHKN 120  
QY 121 LQEHFSDQDLVFLLLTPSIITSCSTHRLHSLYKPKGLFHRVPLVAVANLGMSEQLGYK 180  
DB 121 LQEHFSDQDLVFLLLTPSIITSCSTHRLHSLYKPKGLFHRVPLVAVANLGMSEQLGYK 180  
QY 181 TVSGSCMTGFSRAVQTHSSKFFEDGSLKEVHKINEMYASIQBELKSIKKVEDSEQAV 240  
DB 181 TVSGSCMTGFSRAVQTHSSKFFEDGSLKEVHKINEMYASIQBELKSIKKVEDSEQAV 240  
QY 241 DKLVKDVNRLKREIEKRRGAQIQAAAREKNIQKDPQENIFLCOALRTFFPNSFHLSCVMS 300  
DB 241 DKLVKDVNRLKREIEKRRGAQIQAAAREKNIQKDPQENIFLCOALRTFFPNSFHLSCVMS 300  
QY 301 LKQNRHVSKSSCNYNHLDVVDNLTLMVHTDIPEASPASTPQIIKHKALDLDLDRWQFKRS 360  
DB 301 LKQNRHVSKSSCNYNHLDVVDNLTLMVHTDIPEASPASTPQIIKHKALDLDLDRWQFKRS 360  
QY 361 RLDDTQDKRSKANTGSSNQDKASKMSPETDEIEKMGFGFYSRSPTF 409  
DB 361 RLDDTQDKRSKANTGSSNQDKASKMSPETDEIEKMGFGFYSRSPTF 409  
RESULT 4  
ID AAB65189 standard; protein; 409 AA.  
AC AAB65189;  
DT 02-APR-2001 (first entry)  
XX Human PRO1013 (UNQ496) protein sequence SEQ ID NO:158.  
XX Human; secreted and transmembrane protein; PRO; cytostatic; cell death;  
XX cancer; chromosomal mapping; gene mapping; tissue typing;  
XX diagnostic assay.  
XX Homo sapiens.  
XX WO200073454-A1.  
XX 07-DEC-2000.  
XX 30-MAR-2000; 2000WO-US008439.  
XX 02-JUN-1999; 99WO-US012252.  
XX 23-JUN-1999; 99US-0141037P.  
XX 07-JUL-1999; 99US-0143048P.  
XX 20-JUL-1999; 99US-0144758P.

Db	181	TVSGSCMTGSPRAVQTHSSKFFEDGSLKEVHKINEMVASYLOEELKSI CKKVEDEQAV	240
QY	241	DKLVKDVNRLKEIEIKRGAQIQAAAREKNIQKDPOENIFLQALRTPFPNSEFLHSCVMS	300
Db	241	DKLVKDVNRLKEIEIKRGAQIQAAAREKNIQKDPOENIFLQALRTPFPNSEFLHSCVMS	300
QY	301	LKNRVKSSSCNHNHLDVVDNLTLWVHTDIPEASPASTPOIIKHKALDLDLRWQFKRS	360
Db	301	LKNRVKSSSCNHNHLDVVDNLTLWVHTDIPEASPASTPOIIKHKALDLDLRWQFKRS	360
QY	361	RLDQTKSKANTGSSNODKASKVSSPETDEIEIKMKGFGEYSRPTF	409
Db	361	RLDQTKSKANTGSSNODKASKVSSPETDEIEIKMKGFGEYSRPTF	409

RESULT 5  
 ABG95861  
 ID ABG95861 standard; protein; 409 AA.  
 XX  
 AC ABG95861;  
 XX  
 XX  
 DT 10-DEC-2002 (first entry)  
 DX  
 DE Human secreted/transmembrane protein PRO1013.  
 XX  
 KW Human; secreted protein; transmembrane protein; antirheumatic;  
 KW antiarthritic; osteopathic; sports-related joint problem;  
 KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2002119130-A1.  
 XX  
 PD 29-AUG-2002.  
 XX  
 PF 06-DEC-2001; 2001US-00006867.  
 XX  
 PR 29-OCT-1997; 97US-0063435P.  
 PR 29-OCT-1997; 97US-0064215P.  
 PR 22-APR-1998; 98US-0082797P.  
 PR 29-APR-1998; 98US-0083495P.  
 PR 15-MAY-1998; 98US-0085579P.  
 PR 02-JUN-1998; 98US-0087759P.  
 PR 04-JUN-1998; 98US-0088021P.  
 PR 04-JUN-1998; 98US-0088029P.  
 PR 04-JUN-1998; 98US-0088030P.  
 PR 10-JUN-1998; 98US-0088734P.  
 PR 10-JUN-1998; 98US-0088740P.  
 PR 10-JUN-1998; 98US-0088811P.  
 PR 10-JUN-1998; 98US-0088824P.  
 PR 10-JUN-1998; 98US-0088825P.  
 PR 11-JUN-1998; 98US-0088863P.  
 PR 12-JUN-1998; 98US-0089105P.  
 PR 16-JUN-1998; 98US-0089514P.  
 PR 17-JUN-1998; 98US-0089653P.  
 PR 19-JUN-1998; 98US-0089952P.  
 PR 22-JUN-1998; 98US-0090246P.  
 PR 24-JUN-1998; 98US-0090444P.  
 PR 25-JUN-1998; 98US-0090688P.  
 PR 25-JUN-1998; 98US-0090896P.  
 PR 26-JUN-1998; 98US-0090862P.  
 PR 02-JUL-1998; 98US-0091628P.  
 PR 10-AUG-1998; 98US-0096012P.  
 PR 17-AUG-1998; 98US-0096757P.  
 PR 18-AUG-1998; 98US-0096949P.  
 PR 18-AUG-1998; 98US-0096959P.  
 PR 26-AUG-1998; 98US-0097971P.  
 PR 26-AUG-1998; 98US-0097979P.  
 PR 01-SEP-1998; 98US-0098749P.  
 PR 10-SEP-1998; 98US-0099741P.  
 PR 10-SEP-1998; 98US-0099763P.  
 PR 10-SEP-1998; 98US-0099792P.

26-JUL-1999; 99US-0145698P.  
 28-JUL-1999; 99US-0146222P.  
 17-AUG-1999; 99US-0149396P.  
 15-SEP-1999; 99US-0202109P.  
 15-SEP-1999; 99US-0202154P.  
 08-OCT-1999; 99US-0158663P.  
 30-NOV-1999; 99US-0202831P.  
 01-DEC-1999; 99US-0202830P.  
 16-DEC-1999; 99US-0303009P.  
 20-DEC-1999; 99US-0303091P.  
 05-JAN-2000; 2000US-0000219P.  
 06-JAN-2000; 2000US-0000376P.  
 11-FEB-2000; 2000US-0003565P.  
 18-FEB-2000; 2000US-0004341P.  
 22-FEB-2000; 2000US-0004414P.  
 24-FEB-2000; 2000US-0004914P.  
 24-FEB-2000; 2000US-0005004P.  
 02-MAR-2000; 2000US-0005841P.  
 15-MAR-2000; 2000US-0006884P.  
 20-MAR-2000; 2000US-0007377P.

(GETH ) GENENTECH INC.  
 XX  
 XX  
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PU;  
 PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
 PI Zhang Z;  
 XX  
 WIPI; 2001-032160/04.  
 DR N-PSDB; AAF44145.  
 XX  
 PT PRO polynucleotides used to produce polypeptides used to target bioactive  
 PT molecules such as toxins, radiolabels or antibodies, to specific cells,  
 PT to cause targeted cell death.  
 XX  
 XX  
 PS Claim 12; Fig 95; 935pp; English.  
 XX  
 CC The present invention describes human secreted and transmembrane PRO  
 CC proteins. The PRO proteins have cytostatic activity. The PRO proteins can  
 CC be used for targeted delivery of bioactive molecules, such as toxins,  
 CC radiolabels or antibodies, that cause cell death. PRO nucleotide  
 CC sequences, and their fragments, can be used as hybridisation probes, in  
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA and  
 CC DNA. They may also be used to produce transgenic animals which are used  
 CC to develop and screen therapeutically useful reagents. The PRO nucleotide  
 CC and protein sequence can be used for tissue typing and in treating  
 CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to  
 CC AAF44470 represent PCR primers and hybridisation probes used in the  
 CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAF65154 to  
 CC AAF65300 represent human PRO polynucleotide and protein sequences given  
 CC in the exemplification of the present invention  
 XX  
 SQ Sequence 409 AA;  
 XX  
 Query Match 100.0%; Score 409; DB 4; Length 409;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MEGESTSAVLGSLGALAFQHLNTSDTEGFLGVEKGAENKSDTSDQMDVVEVYITD 60  
 Db 1 MEGESTSAVLGSLGALAFQHLNTSDTEGFLGVEKGAENKSDTSDQMDVVEVYITD 60  
 QY 61 IQYIPCYQLFSPYNSGVEVNEQALKILSNVKNVGVGKFRHSDQIMTFRLLHKN 120  
 Db 61 IQYIPCYQLFSPYNSGVEVNEQALKILSNVKNVGVGKFRHSDQIMTFRLLHKN 120  
 QY 121 LQHFNSQDLVFLLLPSTITESCSHRLHSLYKPKGLFHRVPLVAVANLGMVQLGYK 180  
 Db 121 LQHFNSQDLVFLLLPSTITESCSHRLHSLYKPKGLFHRVPLVAVANLGMVQLGYK 180  
 QY 181 TVSGSCMTGSPRAVQTHSSKFFEDGSLKEVHKINEMVASYLOEELKSI CKKVEDEQAV 240

CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,  
CC H or I polypeptide is labeled with a detectable label or is attached to a  
CC solid support. The proteins are useful for linking a bioactive molecule  
CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,  
CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.  
CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,  
CC or I, or antibodies against them are useful for modulating a biological  
CC activity of a cell expressing a polypeptide designated as A, B, C or D or  
CC E, F, G, H, or I. The cell is killed. The proteins are useful for  
CC identifying agonists or antagonists, for the preparation of a medicament  
CC useful in the treatment of a condition which is responsive to the  
CC proteins, as molecular weight markers for protein electrophoresis  
CC purposes, and as therapeutic agents for treating sports-related joint  
CC problems, articular cartilage defects, osteoarthritis or rheumatoid  
CC arthritis. Nucleic acids encoding the proteins are useful as  
CC hybridisation probes, in chromosome and gene mapping, in the generation  
CC of anti-sense RNA and DNA, for the preparation of the proteins, to  
CC generate transgenic or knockout animals which are useful in the  
CC development and screening of therapeutic useful reagents, for chromosome  
CC identification, and in gene therapy. The antibody is useful as a  
CC therapeutic agent, in a diagnostic assay and for affinity purification of  
CC the protein from recombinant cell culture natural sources. The present  
CC sequence represents a novel secreted or transmembrane protein of the  
CC invention  
XX  
XX Sequence 409 AA;  
SQ  
Query Match 100.0%; Score 409; DB 5; Length 409;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MEGESTSAVLISGFLGALAFQHLNTDSTDEGFLGKVGKAKNSITDSQMDVVEVVTID 60  
Db 1 MEGESTSAVLISGFLGALAFQHLNTDSTDEGFLGKVGKAKNSITDSQMDVVEVVTID 60  
QY 61 IQYIFCYQLFSPYNSGVEVNEQALKKILSNVKNVGVYKFRHSDQIMTFRERLLHKN 120  
Db 61 IQYIFCYQLFSPYNSGVEVNEQALKKILSNVKNVGVYKFRHSDQIMTFRERLLHKN 120  
QY 121 LQEHFNSQDLVFLLLTPSIITSCSTHRLHSLYKPKGLFHRVPLVAVNLGMSQGLYK 180  
Db 121 LQEHFNSQDLVFLLLTPSIITSCSTHRLHSLYKPKGLFHRVPLVAVNLGMSQGLYK 180  
QY 181 TVSGSCMSTGFSRAVQTHSSKFFEDGSLKEVHKINEMVASYLQELKSI CKKYDESEQAV 240  
Db 181 TVSGSCMSTGFSRAVQTHSSKFFEDGSLKEVHKINEMVASYLQELKSI CKKYDESEQAV 240  
QY 241 DKLVKDVNRLKREIKRGAQIOAREKNIQKDPQENIFLQALRTFFPNSEFLHSCVMS 300  
Db 241 DKLVKDVNRLKREIKRGAQIOAREKNIQKDPQENIFLQALRTFFPNSEFLHSCVMS 300  
QY 301 LKNRHYKSSCNVNHLDVVDNLTLVVEHTDIPASPASTPQIIKHKALDLDLRWQFKRS 360  
Db 301 LKNRHYKSSCNVNHLDVVDNLTLVVEHTDIPASPASTPQIIKHKALDLDLRWQFKRS 360  
QY 361 RLDDTQDKRSKANTGSSNODKASKMSSPETDEIERKMGFGYSRSPTF 409  
Db 361 RLDDTQDKRSKANTGSSNODKASKMSSPETDEIERKMGFGYSRSPTF 409  
RESULT 6  
ABUS8466  
ID ABUS8466 standard; protein; 409 AA.  
XX  
AC ABUS8466;  
XX  
DT 15-APR-2003 (first entry)  
XX  
DE Human PRO polypeptide #67.  
XX  
KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;  
KW dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;  
KW antibody-dependent enzyme mediated prodrug therapy.

PR 10-SEP-1998; 98US-0099812P.  
PR 16-SEP-1998; 98US-0099815P.  
PR 16-SEP-1998; 98US-0100627P.  
PR 16-SEP-1998; 98US-0100662P.  
PR 17-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98US-0100683P.  
PR 17-SEP-1998; 98US-0100684P.  
PR 17-SEP-1998; 98US-0100930P.  
PR 22-SEP-1998; 98US-0101279P.  
PR 23-SEP-1998; 98US-0101479P.  
PR 24-SEP-1998; 98US-0101738P.  
PR 24-SEP-1998; 98US-0101743P.  
PR 24-SEP-1998; 98US-0101916P.  
PR 30-SEP-1998; 98US-0102570P.  
PR 06-OCT-1998; 98US-0103449P.  
PR 08-MAR-1999; 98WO-US005028.  
PR 14-MAY-1999; 98WO-US010733.  
PR 02-JUN-1999; 98WO-US012252.  
PR 01-SEP-1999; 98WO-US020111.  
PR 15-SEP-1999; 98WO-US021090.  
PR 15-SEP-1999; 98WO-US021194.  
PR 22-DEC-1999; 98WO-US030720.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 02-MAY-2000; 2000WO-US014042.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032378.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 30-MAY-2001; 2001WO-US017443.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
XX Grimaldi JC, Gurney AL, Watanabe CK, Wood WI,  
XX N-PSDB; ABS74388.  
XX  
XX WPI; 2002-731348/79.  
XX  
XX N-PSDB; ABS74388.  
XX  
XX New isolated secreted and transmembrane PRO polypeptide useful for  
XX modulating biological activity of a cell, or for treating sports-related  
XX joint problems, osteoarthritis or rheumatoid arthritis.  
XX  
XX Claim 20; Fig 22; 399pp; English.  
XX  
XX The invention relates to an isolated secreted and transmembrane PRO  
XX polypeptide having 80 % sequence identity to a sequence appearing as  
XX ABG95851-ASG95934 or their associated signal peptide, or a sequence of an  
XX extracellular domain of the proteins with their associated signal peptide  
XX or lacking its associated signal peptide. Also included are the nucleic  
XX acids encoding the proteins, vectors, host cells, fusion proteins and  
XX antibodies which specifically bind to the proteins. The proteins are  
XX useful for detecting a polypeptide designated as A, B, C or D in a sample  
XX suspected of containing an A, B, C or D polypeptide, by contacting the  
XX sample with a polypeptide designated as E, F, G, H or I (or vice versa)  
XX and determining the formation of a A/E, E/F, B/G, C/H or D/I polypeptide  
XX conjugate in the sample, where the formation of the conjugate is  
XX indicative of the presence of an A, B, C or D polypeptide in the sample,  
XX where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a  
XX PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801  
XX polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a  
XX PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises

XX	Homo sapiens.	PR	04-JUN-1998;	98US-0088029P.
OS		PR	04-JUN-1998;	98US-0088033P.
XX		PR	04-JUN-1998;	98US-0088326P.
XX	US2003027272-A1.	PR	05-JUN-1998;	98US-0088167P.
XX		PR	05-JUN-1998;	98US-0088202P.
PD		PR	05-JUN-1998;	98US-0088212P.
XX	06-FEB-2003.	PR	05-JUN-1998;	98US-0088217P.
XX		PR	09-JUN-1998;	98US-0088655P.
PF		PR	10-JUN-1998;	98US-0088722P.
XX	21-JUN-2002; 2002US-00176492.	PR	10-JUN-1998;	98US-0088738P.
XX		PR	10-JUN-1998;	98US-0088740P.
PR	18-SEP-1997;	PR	10-JUN-1998;	98US-0088811P.
PR	18-SEP-1997;	PR	10-JUN-1998;	98US-0088824P.
PR	17-OCT-1997;	PR	10-JUN-1998;	98US-0088825P.
PR	21-OCT-1997;	PR	10-JUN-1998;	98US-0088828P.
PR	24-OCT-1997;	PR	10-JUN-1998;	98US-0088861P.
PR	24-OCT-1997;	PR	11-JUN-1998;	98US-0088863P.
PR	28-OCT-1997;	PR	11-JUN-1998;	98US-0088876P.
PR	28-OCT-1997;	PR	11-JUN-1998;	98US-0088876P.
PR	29-OCT-1997;	PR	12-JUN-1998;	98US-0089090P.
PR	31-OCT-1997;	PR	12-JUN-1998;	98US-0089105P.
PR	31-OCT-1997;	PR	16-JUN-1998;	98US-0089512P.
PR	13-NOV-1997;	PR	16-JUN-1998;	98US-0089514P.
PR	21-NOV-1997;	PR	17-JUN-1998;	98US-0089538P.
PR	24-NOV-1997;	PR	17-JUN-1998;	98US-0089598P.
PR	24-NOV-1997;	PR	17-JUN-1998;	98US-0089653P.
PR	11-DEC-1997;	PR	18-JUN-1998;	98US-0089908P.
PR	12-DEC-1997;	PR	19-JUN-1998;	98US-0089952P.
PR	17-DEC-1997;	PR	22-JUN-1998;	98US-0090246P.
PR	18-DEC-1997;	PR	22-JUN-1998;	98US-0090252P.
PR	10-MAR-1998;	PR	22-JUN-1998;	98US-0090254P.
PR	11-MAR-1998;	PR	24-JUN-1998;	98US-0090429P.
PR	11-MAR-1998;	PR	24-JUN-1998;	98US-0090435P.
PR	20-MAR-1998;	PR	24-JUN-1998;	98US-0090444P.
PR	27-MAR-1998;	PR	24-JUN-1998;	98US-0090461P.
PR	27-MAR-1998;	PR	24-JUN-1998;	98US-0090535P.
PR	31-MAR-1998;	PR	24-JUN-1998;	98US-0090540P.
PR	31-MAR-1998;	PR	25-JUN-1998;	98US-0090576P.
PR	01-APR-1998;	PR	25-JUN-1998;	98US-0090678P.
PR	01-APR-1998;	PR	25-JUN-1998;	98US-0090688P.
PR	08-APR-1998;	PR	25-JUN-1998;	98US-0090690P.
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PR	15-APR-1998;	PR	25-JUN-1998;	98US-0090695P.
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PR	21-APR-1998;	PR	26-JUN-1998;	98US-0090863P.
PR	22-APR-1998;	PR	01-JUL-1998;	98US-0091359P.
PR	22-APR-1998;	PR	01-JUL-1998;	98US-0091359P.
PR	28-APR-1998;	PR	02-JUL-1998;	98US-0091478P.
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PR	29-APR-1998;	PR	02-JUL-1998;	98US-0091626P.
PR	29-APR-1998;	PR	02-JUL-1998;	98US-0091628P.
PR	29-APR-1998;	PR	02-JUL-1998;	98US-0091632P.
PR	29-APR-1998;	PR	24-JUL-1998;	98US-0094006P.
PR	03-MAY-1998;	PR	04-AUG-1998;	98US-0095282P.
PR	06-MAY-1998;	PR	10-AUG-1998;	98US-0095998P.
PR	07-MAY-1998;	PR	10-AUG-1998;	98US-0096012P.
PR	07-MAY-1998;	PR	17-AUG-1998;	98US-0096757P.
PR	15-MAY-1998;	PR	17-AUG-1998;	98US-0096766P.
PR	15-MAY-1998;	PR	17-AUG-1998;	98US-0096867P.
PR	15-MAY-1998;	PR	17-AUG-1998;	98US-0096891P.
PR	18-MAY-1998;	PR	17-AUG-1998;	98US-0096897P.
PR	22-MAY-1998;	PR	18-AUG-1998;	98US-0096949P.
PR	22-MAY-1998;	PR	18-AUG-1998;	98US-0096959P.
PR	28-MAY-1998;	PR	18-AUG-1998;	98US-0097022P.
PR	28-MAY-1998;	PR	26-AUG-1998;	98US-0097952P.
PR	02-JUN-1998;	PR	26-AUG-1998;	98US-0097955P.
PR	02-JUN-1998;	PR	26-AUG-1998;	98US-0097955P.
PR	03-JUN-1998;	PR	26-AUG-1998;	98US-0097971P.
PR	04-JUN-1998;	PR	26-AUG-1998;	98US-0097971P.
PR	04-JUN-1998;	PR	26-AUG-1998;	98US-0098014P.
PR	04-JUN-1998;	PR	01-SEP-1998;	98US-0098716P.





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PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 15-MAY-1998; 98US-0085573P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085700P.
PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087208P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088722P.
PR 10-JUN-1998; 98US-0088718P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088863P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089090P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089922P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090461P.
PR 24-JUN-1998; 98US-0090535P.
PR 24-JUN-1998; 98US-0090540P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
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KW tissue typing.  
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KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;  
KW chondrocyte; proliferation; differentiation; cartilage disorder;  
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;  
KW adrenal tumour; lung; colon; breast; prostate; kidney; cervix;  
KW liver; drug screening; transgenic animal; genetic analysis;  
KW antiarthritic; vulnery; gene therapy.  
XX  
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XX  
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PD 06-FEB-2003.  
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PD 27-FEB-2003.  
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PR 24-AUG-2000; 2000WO-US033328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
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PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 28-AUG-2001; 2001US-00941992.  
XX (GETH) GENENTECH INC.  
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Klijavin IJ, Napier MA, Pan J, Paoni NF;  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
PI Zhang Z;  
XX WPI; 2003-247083/24.  
DR N-PSDB; ABX80226.  
XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
XX and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
XX are therapeutically useful for enhancing immune response and in cancer  
XX treatments.  
XX Claim 12; Fig 95; 648pp; English.  
XX The invention describes an isolated human PRO polypeptide. The PRO  
XX polypeptides are useful in detecting PRO polypeptides in a sample, in  
XX linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
XX in modulating at least one biological activity of a cell expressing a PRO  
XX polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus  
XX useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186  
XX stimulate adrenal cortical capillary endothelial growth, and PRO536,  
XX PRO943, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,  
XX PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus  
XX useful for treating conditions or disorders where angiogenesis would be  
XX beneficial, e.g. wound healing and antagonist of this polypeptide are  
XX useful for treating cancerous tumours. PRO812 inhibits vascular  
XX endothelial growth factor (VEGF) stimulated proliferation of endothelial  
XX cells and is thus useful for inhibiting endothelial cell growth in  
XX mammals which would be beneficial in inhibiting tumour growth. PRO826,  
XX PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of  
XX stimulated T-lymphocytes and are therapeutically useful for enhancing  
XX immune response. PRO828, PRO825, PRO1068 or PRO1132 enhance survival of  
XX retinal neurons cells (PRO1132 is also enhances survival/proliferation of  
XX rod photoreceptor cells) and therefore are useful for treating retinal  
XX disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813  
XX and PRO1066 induce proliferation of mammalian kidney mesangial cells,  
XX and therefore are useful for treating kidney disorders associated with  
XX decreased mesangial cell function such as Berger disease or other  
XX nephropathies associated with dermatitis, herpeticiformis or Crohn's  
XX disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the  
XX proliferation and/or redifferentiation of chondrocytes in culture and are  
XX thus useful for treating sports injuries, and arthritis. This is the  
XX amino acid sequence of a novel human PRO protein  
XX Sequence 409 AA;  
XX Query Match 100.0%; Score 409; DB 6; Length 409;  
XX Best Local Similarity 100.0%; Pred. No. 0;  
XX Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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XX AC ABU82594;  
XX DT 26-JUN-2003 (first entry)  
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XX cardiac insufficiency disorders; angiogenesis; wound healing;  
XX cancerous tumour; immune response; retinal disorder; sight loss;  
XX retinitis pigmentosa; age-related macular degeneration; AMD;  
XX kidney disorder; Berger disease; nephropathy; dermatitis; herpeticiformis;  
XX Crohn's disease; sports injury; arthritis.  
XX Homo sapiens.  
XX US2003032023-A1.  
XX 13-FEB-2003.  
XX 14-NOV-2001; 2001US-00990711.  
XX 16-JUN-1997; 97US-0049787P.  
XX 17-OCT-1997; 97US-0062250P.  
XX 05-NOV-1997; 97WO-US020069.  
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XX 13-NOV-1997; 97US-0065311P.  
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XX 25-FEB-1998; 98US-0075945P.  
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XX 09-JUN-1998; 98US-0088655P.

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PR	18-FEB-2000;	2000WO-US004341
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PR	10-MAR-2000;	2000WO-US006319
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AC ABU82772;
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DT 27-JUN-2003 (first entry)
XX
DE Human PRO polypeptide #67.
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KW Human; PRO polypeptide; secreted and transmembrane protein; tumour;
XX chromosome mapping; Gene mapping; cytostatic.
XX
OS Homo sapiens.
XX
PN US2003032113-A1.
XX
PD 13-FEB-2003.
XX
PF 20-JUN-2002; 2002US-00176911.
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PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0098014P.
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099602P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099812P.
PR 15-SEP-1998; 98US-0100388P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 16-SEP-1998; 98US-0101751P.
PR 16-SEP-1998; 98US-0101933P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101475P.

PR 23-SEP-1998; 98US-0101477P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101739P.
PR 24-SEP-1998; 98US-0101743P.
PR 25-SEP-1998; 98US-0101922P.
PR 25-SEP-1998; 98US-0101786P.
PR 29-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102965P.
PR 05-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98US-0103395P.

Query Match 100.0%; Score 409; DB 6; Length 409;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEGESTSAVLGSGFVLGALAFQHLNLTSDTEGFLGVEKGEAKNSITDSQMDVVEVYITD 60
Db 1 MEGESTSAVLGSGFVLGALAFQHLNLTSDTEGFLGVEKGEAKNSITDSQMDVVEVYITD 60
Qy 61 IQKYIPCYQLFSFYNSSGVEVNEQALKKILSNVKNVGVGYKFRHSDQIMTFRERLLHKN 120
Db 61 IQKYIPCYQLFSFYNSSGVEVNEQALKKILSNVKNVGVGYKFRHSDQIMTFRERLLHKN 120
Qy 121 LQEHFNSQDLVFLLLTPSIITSCSTRLEHSLYKPKQLFHRVPLVAVANLGMSEQLGYK 180
Db 121 LQEHFNSQDLVFLLLTPSIITSCSTRLEHSLYKPKQLFHRVPLVAVANLGMSEQLGYK 180
Qy 181 TVSSGCMSTGFSRAVQTHSSKPFEDGSLKEVHKINEMVASIQEELKSI CKKVEDSEQAV 240
Db 181 TVSSGCMSTGFSRAVQTHSSKPFEDGSLKEVHKINEMVASIQEELKSI CKKVEDSEQAV 240
Qy 241 DKLVKDVNRLKREIKRGAQIOAREKNIQKDPQENIFLCOALRTFFPNSEFLHSCVMS 300
Db 241 DKLVKDVNRLKREIKRGAQIOAREKNIQKDPQENIFLCOALRTFFPNSEFLHSCVMS 300
Qy 301 LKNRHSVKSNCYNHLLDVVDNLTLVVEHTDPEASPASTPQIIKHKALDLDNRWQFKRS 360
Db 301 LKNRHSVKSNCYNHLLDVVDNLTLVVEHTDPEASPASTPQIIKHKALDLDNRWQFKRS 360
Qy 361 RLDDTQDKRSKANTGSSNQDKASKMSSPETDEIEKMGFGEYSRSPTF 409
Db 361 RLDDTQDKRSKANTGSSNQDKASKMSSPETDEIEKMGFGEYSRSPTF 409

RESULT 16
ABUS9893
ID ABUS9893 standard; protein; 409 AA.
XX AC ABUS9893;
XX DT 11-AUG-2003 (first entry)
XX DE Novel human secreted and transmembrane protein PRO1013.
XX KW Human; gene therapy; tissue typing; tumour; chondrocyte proliferation;
XX KW chondrocyte differentiation; tumour necrosis factor-alpha release;
XX KW affinity purification.
XX OS Homo sapiens.
XX PN US2003036147-A1.
XX 20-FEB-2003.
```



PR	10-SEP-1998;	98US-0099754P.	Query Match	100.0%;	Score 409;	DB 6;	Length 409;
PR	10-SEP-1998;	98US-0099763P.	Best Local Similarity	100.0%;	Pred. No. 0;		
PR	10-SEP-1998;	98US-0099812P.	Matches 409;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
PR	15-SEP-1998;	98US-0100388P.					
PR	16-SEP-1998;	98US-0100662P.					
PR	16-SEP-1998;	98US-0100664P.					
PR	16-SEP-1998;	98US-0101751P.					
PR	16-SEP-1998;	98US-0101933P.					
PR	17-SEP-1998;	98US-0100683P.					
PR	17-SEP-1998;	98US-0100684P.					
PR	17-SEP-1998;	98US-0100919P.					
PR	17-SEP-1998;	98US-0100930P.					
PR	18-SEP-1998;	98US-0100849P.					
PR	18-SEP-1998;	98US-0101014P.					
PR	18-SEP-1998;	98US-0101068P.					
PR	23-SEP-1998;	98US-0101471P.					
PR	23-SEP-1998;	98US-0101472P.					
PR	23-SEP-1998;	98US-0101475P.					
PR	23-SEP-1998;	98US-0101477P.					
PR	24-SEP-1998;	98US-0101738P.					
PR	24-SEP-1998;	98US-0101739P.					
PR	24-SEP-1998;	98US-0101743P.					
PR	25-SEP-1998;	98US-0101922P.					
PR	25-SEP-1998;	98US-0101786P.					
PR	29-SEP-1998;	98US-0102207P.					
PR	29-SEP-1998;	98US-0102240P.					
PR	29-SEP-1998;	98US-0102330P.					
PR	29-SEP-1998;	98US-0102331P.					
PR	30-SEP-1998;	98US-0102487P.					
PR	30-SEP-1998;	98US-0102570P.					
PR	30-SEP-1998;	98US-0102571P.					
PR	01-OCT-1998;	98US-0102684P.					
PR	01-OCT-1998;	98US-0102687P.					
PR	02-OCT-1998;	98US-0102965P.					
PR	06-OCT-1998;	98US-0103258P.					
PR	06-OCT-1998;	98US-0103449P.					
PR	07-OCT-1998;	98US-00168978.					
QY	1	MEGESTSAVLSGFLGALAFQHLNLTDSDETEGFLGGEVKEAKNSITDSQMDDEVVYITD 60					
Db	1	MEGESTSAVLSGFLGALAFQHLNLTDSDETEGFLGGEVKEAKNSITDSQMDDEVVYITD 60					
QY	61	IQKIYPCYOLFSPYNSGGEVNEQALKILSNVKNVGVWYKFRHSDDQIMTFRELLHKN 120					
Db	61	IQKIYPCYOLFSPYNSGGEVNEQALKILSNVKNVGVWYKFRHSDDQIMTFRELLHKN 120					
QY	121	LQEHFNSQDLVFLLTTPSIITSCSTHRLHSLYKPKGLFHRVPLVNVANLGMSEQLGYK 180					
Db	121	LQEHFNSQDLVFLLTTPSIITSCSTHRLHSLYKPKGLFHRVPLVNVANLGMSEQLGYK 180					
QY	181	TVSGSCMSTGFGRAVQTHSSKTFEEDGSLKVEHKINEMVASYLQELKSIKKVEDSEQAV 240					
Db	181	TVSGSCMSTGFGRAVQTHSSKTFEEDGSLKVEHKINEMVASYLQELKSIKKVEDSEQAV 240					
QY	241	DKLVKDVNLKBEIEKRGQAOTQAREKNIQKDPQENIFLCOALTFEPNSEFLHSCVMS 300					
Db	241	DKLVKDVNLKBEIEKRGQAOTQAREKNIQKDPQENIFLCOALTFEPNSEFLHSCVMS 300					
QY	301	LKNRHSVKSVCNNYHLDVVNDLTLVHTDIPASPASTPQIIXKALDLDLRWQFKRS 360					
Db	301	LKNRHSVKSVCNNYHLDVVNDLTLVHTDIPASPASTPQIIXKALDLDLRWQFKRS 360					
QY	361	RLLDQDKRSKANTGSSNQDKASKSSPTDEIEKMGFGYSRSPTF 409					
Db	361	RLLDQDKRSKANTGSSNQDKASKSSPTDEIEKMGFGYSRSPTF 409					

RESULT 17  
ABR68142

ID	ABR68142 standard; protein; 409 AA.
XX	ABR68142;
AC	
XX	
DT	11-AUG-2003 (first entry)
XX	Human secreted polypeptide PRO1013, SEQ ID NO:134.
DE	
XX	Human; PRO; secreted protein; transmembrane protein;
XX	extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW	chondrocyte; proliferation; differentiation; cartilage disorder;
KW	bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW	adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW	liver; drug screening; transgenic animal; genetic analysis;
KW	antiarthritic; vulnery; gene therapy.
OS	Homo sapiens.
XX	
XX	US2003027264-A1.
PN	
XX	06-FEB-2003.
PD	
XX	18-JUN-2002; 2002US-00174579.
PF	
XX	18-SEP-1997; 97US-0059263P.
PR	18-SEP-1997; 97US-0059266P.
PR	17-OCT-1997; 97US-0062250P.
PR	21-OCT-1997; 97US-0063486P.
PR	24-OCT-1997; 97US-0063120P.
PR	24-OCT-1997; 97US-0063121P.
PR	28-OCT-1997; 97US-0063540P.
PR	28-OCT-1997; 97US-0063541P.
PR	28-OCT-1997; 97US-0063544P.
PR	28-OCT-1997; 97US-0063564P.
PR	29-OCT-1997; 97US-0063734P.
PR	31-OCT-1997; 97US-0063870P.
PR	31-OCT-1997; 97US-0064103P.
PR	13-NOV-1997; 97US-0065311P.
PR	21-NOV-1997; 97US-0066120P.
PR	24-NOV-1997; 97US-0066466P.
PR	24-NOV-1997; 97US-0066772P.
PR	11-DEC-1997; 97US-0069335P.
PR	12-DEC-1997; 97US-0069425P.
PR	17-DEC-1997; 97US-0069870P.
PR	18-DEC-1997; 97US-0068017P.
PR	10-MAR-1998; 98US-0077450P.
PR	11-MAR-1998; 98US-0077632P.
PR	11-MAR-1998; 98US-0077649P.
PR	20-MAR-1998; 98US-0078866P.
PR	20-MAR-1998; 98US-0078939P.
PR	27-MAR-1998; 98US-0079664P.
PR	27-MAR-1998; 98US-0079786P.
PR	31-MAR-1998; 98US-0080107P.
PR	31-MAR-1998; 98US-0080194P.
PR	01-APR-1998; 98US-0080327P.
PR	01-APR-1998; 98US-0080333P.
PR	08-APR-1998; 98US-0081049P.
PR	08-APR-1998; 98US-0081070P.
PR	09-APR-1998; 98US-0081195P.
PR	15-APR-1998; 98US-0081938P.
PR	21-APR-1998; 98US-0082568P.
PR	21-APR-1998; 98US-0082569P.
PR	22-APR-1998; 98US-0082704P.
PR	22-APR-1998; 98US-0082797P.
PR	28-APR-1998; 98US-0083222P.
PR	29-APR-1998; 98US-0083495P.
PR	29-APR-1998; 98US-0083496P.
PR	29-APR-1998; 98US-0083499P.
PR	29-APR-1998; 98US-0083559P.
PR	05-MAY-1998; 98US-0084366P.
PR	06-MAY-1998; 98US-0084414P.
PR	07-MAY-1998; 98US-0084639P.
PR	07-MAY-1998; 98US-0084640P.